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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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mode1 ws bujsn protein search, 1 protein

December 1, 2004, 12:07:39 ; Search time 80.3158 Seconds (without alignments) 1561.731 Million cell updates/sec Run on:

US-09-095-478A-7_COPY_188_405 score: Title: Perfect

QNRDKNRYRDILPYDSTRVP.....DIMNIVTQMRKQRCGMIQTK 218 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	O55082 mus musculu	Q9y406 homo sapien		Q64512 mus musculu	Q12923 homo sapien			Q8n4s3 homo sapien	homo	Q9wu22 mus musculu			Q8my42 eptatretus			Q8my41 eptatretus		Q9jj07 mus musculu	Q6mzf6 homo sapien	Cae46198 homo sapi	рошо	homo	Q12913 homo sapien		Q6dch9 xenopus lae	Aah70687 xenopus l	Q8k3q2 mus musculu	Q9ibd8 cyprinus ca		**	Q62884 rattus norv
SUMMARIES	αI	055082	Q9Y406	Q28006	PIND MOUSE	PTND_HUMAN	<u> Фекн</u>	Q6GPK7	Q8N4S3	PTN3 HUMAN	Q9WUZ2	Q8MY44	Q8MY45	Q8MY42	Q8MY43	QBCIW2	Q8MY41	Q80VN7	707707	Q6MZF6	CAE46198	PTPB_HUMAN	PIN4 HUMAN	PTPJ HUMAN	Q6NRP9	Ферсив	AAH70687	Q8K3Q2	Q91BD8	PTNS_HUMAN	044328	Q62884
	DB	2	7	7	Н	-	N	7	7	-	7	~	7	7	7	~	7	7	0	~	7	Н	Н	Н	7	~	7	7	7	Н	~	7
	Query Match Length	426	398	2484	2453	2485	2500	920	292	913	926	1222	1100	1187	1202	1998	907	1102	579	1956	1956	1997	926	1337	929	929	929	1238	1216	94		1216
d	Query Match	100.0	79.0	47.4	46.9	46.1		40.8					38.5											37.8		37.6	37.6	37.4	37.4		37.3	37.2
	Score	1174	928	556.5	550.5	541.5	541.5	479	468	467	461.5	453.5	452.5		452.5			447.5		445.5	445.5	445.5	444.5	444	441.5	441.5	441.5	439	438.5	m	437.5	437
	Result No.	-	7	٣	4	S	ø	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

Q61373 mus musculu	Q06180 mus musculu	Q922e7 mus musculu	Q64455 mus musculu	Aak96030 mus muscu	Q9iba0 potamotrygo	Q9iai8 xenopus lae	Q96au5 homo sapien	P35233 rattus norv	P17706 homo sapien	P35822 mus musculu	Q9iba2 potamotrygo	Q9um81 homo sapien	P23468 homo sapien
Q61373	PIN2 MOUSE	Q922 <u>E</u> 7	PTPJ MOUSE	AAK96030	Q9IBA0	Q9IAI8	Q96AUS	PIN2 RAT	PTN2 HUMAN	PTPK MOUSE	Q9IBA2	Q9UM81	PTPD_HUMAN
7	Н	~	~	7	7	7	7	Н	-	Н	7	7	Н
361	382	406	1238	1238	468	615	353	363	415	1457	468	1502	1912
37.1	37.1	37.1	37.1	37.1	37.0	37.0	37.0	37.0	37.0	37.0	36.8	36.8	36.8
436	436	436	436	436	434.5	434.5	434	434	434	434	432.5	432.5	432.5

ALIGNMENTS

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SEQUENCE FROM N.A.
STRANDE-SCSPLAG, TISSUE-Testis;
The FANTOM CONSortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I and I Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Testis; STRAIN=C57BL/6J; TISSUE=1042159; MEDLINE=2049974; PubMed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Komno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to
                                                                   01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 26, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Protein-tyrosine-phosphatase (EG 3.1.3.48) (Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4921505B14
product:protein tyrosine phosphatase, non-receptor type 20, full
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
STRAIN=C57BL/6J; TISSUE=11217851;
RIKEN FANTOM COnsortium;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                           TISSUE=Testis;
MEDLINE=98070510; PubMed=9407093;
Ohsugi M., Kuramochi S., Matsuda S., Yamamoto T.;
"Molecular cloning and characterization of a novel cytoplasmic protein-tyrosine phosphatase that is specifically expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=99279253; Pubmed=10349636;
Cardinci P., Hayashizaki Y.;
Cardinci Ficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                   426 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem. 272:33092-33099(1997)
                                   PRT;
                                   PRELIMINARY;
                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                     insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                     spermatocytes.";
                                                                                                                                                                                                  Name=Ptpn20;
                                                        055082
                                   055082
RESULT 1
055082
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PRELIMINARY;

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STRAIN-CSTBL/GAJ; TISSUB=Testis;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Adachi J., Puruno M., Hanagaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu W., Hiramoto K., Hiraoka T., Hirozane T.,
An Hayashida K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Saaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A Saaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
A Tagawa A., Takahashi F., Takaku. Akahira S., Takeda Y., Tanaka T.,
A Tagawa A., Takahashi F., Takaku. A., Muramatsu M., Hayashizaki Y.;
A Tagawa A., Takahashi F., Takaku. A., Muramatsu M., Hayashizaki Y.;
A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
B Shibited (JUL-2001) to the EMBL/GenBank/DDBJ databases.
B RBL; D64141; BAA237611.1 -
B RBL; D64141; BAA237611.1 -
B RBL; D6404725; Fiprotein tyrosine phosphatase activity; IEA.
GO; GO:00064729; Fiprotein amino acid dephosphorylation; IEA.
GO; GO:0006472; Fiprotein amino acid dephosphorylation; IEA.
B RRNT; SM00102; Y Phosphatase.
B RRNT; SM00102; Y Phosphatase.
B RRNT; SM00102; Y Phosphatase.
B RRNT; SM00103; TYR PHOSPHATASE 1; 1.
B RRNTT; PROSOTE; FYR PHOSPHATASE 2; 1.
B RRNSTIE; PS50056; TYR PHOSPHATASE 2; 1.
B RRNSTIE; PS50056; TYR PHOSPHATASE 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ
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                                                                                                                    STRAIN=CS7BL/64); TISSUB=Testis;

MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Itoh M., Sumi N., Ishii K., Hazama M., Nishine T., Harada A., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa W., Diara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rikik integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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100.0%; Pred. No. 1.8e-106;
ive 0; Mismatches 0;
                                   Senome Res. 10:1617-1630(2000)
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Matches 218; Conservative
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                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                     Ansorge W., Witcher U., Mewes H.W., Gassenhuber J., Wiemann S.;
Ansorge W., Witcher U., Mewes H.W., Gassenhuber J., Wiemann S.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
REMBL, ALGO040; CAB43248.1; -.
REMBL, ALGO040; CAB43248.1; -.
REMBL, ALGO040; CAB43248.1; -.
REMBL, CONDIGONO, TOWN CONDIGONO, TEA.
GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
GO; GO:0004725; F:protein amino acid dephosphorylation; IEA.
RO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
RO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
REMIS: PRO0002; Tyrepper P.P.
REMIS: ROOONO; PRYPAPHTASE.
REMART; SMO0194; PTPC; 1.
REMOSITE; ROSO0386; TYR PHOSPHATASE.1; 1.
REMOSITE; PSSO066; TYR PHOSPHATASE.2; 1.
REMOSITE; PSSO065; TYR PHOSPHATASE.2; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.0%; Score 928; DB 2; Length 398; 77.9%; Pred. No. 2.2e-82; ive 24; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vega Q.C., Walton K.M., Dixon J.E.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 5 PDZ/DHR domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            398 AA; 45690 MW; 857AAD03747870A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Last sequence upd 01-UUN-2003 (TrEMBLrel. 24, Last annotation u Hypothetical protein DKFZp566K0524 (Fragment) Name-DKFZp566K0524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Created)
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U20807; AAA73516.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 77.9%
Matches 169; Conservative
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                                                                                                               Homo sapiens (Human)
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                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                TISSUE=Kidney;
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PIR;
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PIR;
PDB;
2235 ENRRKORYKNILPYDATRVPLGDEGGYINASFIKIPVGREEFVYIACQGPLPTTVGDFWQ 2294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2295 MIWEQNSSVIAMMTQEVEGEKIKCQRYWPNVLGKSTMVSNRLRLALVRVQQLKGFVVRAM 2354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 MVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFTVRVF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 QIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2484;
                 GO; GO:0005856, C:cytoskeleton; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:00016787; F:protein binding; IEA.
GO; GO:0004725, F:protein tyrosine phosphatase activity; IEA.
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
InterPro; IPR000299; Band_4.1.
InterPro; IPR001909; Kinase_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276382 MW; 45A92F0D4F1ED13D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2415 GTLICIDVVLGLISQDLEFDISDLVRCMRLQRHGMVQTE 2453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVFICVDVVFSAIEKNYSFDIMNIVTOMRKORCGMIQTK 218
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PROSITE; PSO0661; FERM 2; FALSE NEG.
PROSITE; PSSO057; FERM 3; 1.
PROSITE; PSO0106; PDZ, 3; 1.
PROSITE; PSO0383; TYR PHOSPHATASE 1; FALSE NEG.
PROSITE; PSSO056; TYR PHOSPHATASE 2; 1.
PROSITE; PSSO055; TYR_PHOSPHATASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.4%; Score 556.5;
48.4%; Pred. No. 5.7
                                                                                                                                                                                                     InterPro: IPR001478; PDZ.
InterPro: IPR001036; PH related.
InterPro: IPR000387; TYR_phosphatase.
InterPro: IPR000242; TYR_PP.
Pfam; PF00373; Band_41; I.
Pfam; PF00102; Y_phosphatase; I.
PRINTS; PR00935; BAND41.
PRINTS; PR00700; PRTYPHPHTASE.
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STRAIN=C57BL/6; TISSUE=Skin;
MEDLINE=96340953; PubMed=8749712;
                                                                                                                                                                 InterPro; IPR011009; Kinase_like.
InterPro; IPR011019; KIND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 48.4
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00295; B41; 1.
SMART; SM00750; KIND; 1.
SMART; SM00228; PDZ; 5.
SMART; SM00194; PTPC; 1.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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-: SUBUNIT: Binds PLEKHA1 and PLEKHA2 through its first PDZ domain

-: SUBUNIT: Binds PLEKHA1 and PLEKHA2 through its first PDZ domain.

-: SUBUNIT: Binds PLEKHA1 and PLEKHA2 through its receptor)

-: SUBCHILLIAN LOCATION: Obtains the second and fourth PDZ domains.

-: SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-: SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

-: SIMILARITY: Belongs to the protein-tyrosine phosphatase family.

Non-receptor class subfamily.

-: SIMILARITY: Contains 5 PDZ/DHR domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98155214; PubMed=9487134; Cuppen E., Gerrits H., Pepers B., Wieringa B., Hendriks W.; Papers B., Morife in Prb-BL and RIL bind to internal protein segments in the LIM domain protein RIL."; Mol. 861. (2011 9:671-683 (1998).
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Hendriks W., Schepens J., Baechner D., Rijss J., Zeeuwen P., Zechner U., Hameister H., Mieringa B.;
M. Hameister H., Mieringa B.;
"Molecular cloning of a mouse epithelia! protein-tyrosine phosphatase with similarities to submembranous proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: Regulates negatively PAS-induced apoptosis and NGFR-mediated pro-apoptotic signaling.
                                                                                                                                                                                                                                                                   STRAIN=DBA/2;
MEDINE=591516; PubMed=7843407;
MEDINE=591516; PubMed=7843407;
Matanabe T., Mikouyama Y., Tabata S., Nomura N., Thomas M.,
Watanabe T., Oishi M.;
"Characterization Of a protein tyrosine phosphatase (RIP) expressed a very early stage of differentiation in both mouse erythroleukemia and embryonal carcinoma cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sawada M., Ogata M., Fujino Y., Hamaoka T.; "CDNA cloning of a novel protein tyrosine phosphatase with homology cytoskeletal protein 4.1 and its expression in T-lineage cells."; Biochem. Biophys. Res. Commun. 203:479-484 [1994].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BALB/c; TISSUB=Brain;
MEDLINE=95134232; PubMed=7832766;
Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.;
"A novel receptor-type protein tyrosine phosphatase with a single
catalytic domain is specifically expressed in mouse brain.";
Biochem. J. 305:499-504 (1995).
                                                                                                                                                      Cell. Biochem. 59:418-430(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 2267-2373 FROM N.A.
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EMBL; D28529; BAA05895.1;
EMBL; Z23059; CAA80594.1;
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                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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SEQUENCE OF 1216-2490 FROM N.A.
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                                                                                                                                                                                                                                                             phosphatase 1) (FAP-1)
                                                                                                                                                                                                                                                                                               (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                        HUMAN
                                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N -> 1 (in Ref. 2).

K -> E (in Ref. 2).

Q -> K (in Ref. 2).

S -> T (in Ref. 2).

S -> T (in Ref. 2).

R -> Q (in Ref. 2).

QTPHYXDYSFVTEDNT -> KHPMSKTTALLLKII (in Ref. 1).

D -> H (in Ref. 2).

S -> P (in Ref. 2).

N -> I (in Ref. 2).

S -> P (in Ref. 2).

S -> P (in Ref. 2).

S -> P (in Ref. 2).

S -> T (in Ref. 2).

BGLPQ -> GSHSDARQPPKAPP (in Ref. 1).
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CAPSFSN -> TSGTASRAFVSY (in Ref.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein-tyrosine phosphatase. Phosphocysteine intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71; Indels
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                                                                                                                                                                                                                                                                                                           PROSITE; PSDUDG; PDZ; 5.
PROSITE; PSS0186; PDZ; 5.
PROSITE; PSS0183; TYR_PHOSPHATASE_1; FALSE_NEG.
PROSITE; PSS0056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
3D-structure; Coiled Coil; Cytoskeleton; Hydrolase; Protein phosphatase; Repeat; Structural protein.

Protein phosphatase; Repeat; Structural protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.9%; Score 550.5; DB 1
49.5%; Pred. No. 2.2e-44;
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HIRNSNCAPSFSN
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SMART; SM00229; PDZ; 5.
SMART; SM00194; PTPC; 5.
SMART; SM00404; PTPC_motif; 1.
PROSITE; PS00660; PERM 1; FALSE_NEG.
PROSITE; PS00661; FERM 2; FALSE_NEG.
                                                                 Interpro; IPR001478; PDZ.
Interpro; IPR000387; TYR phosphatase.
Interpro; IPR000242; Tyr_PP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDZ 5.
                                                                                                                                                      Pfam; PF00102; Y phosphatase; 1.
PRINTS; PR00935; BAND41.
PRINTS; PR00700; PRTYPHPHTASE.
 PDB; 10ZI; NWR; A=1351-1444.
MGD; MGI:102293; PCPD13.
INCETPC; IPR000299; Band 4.1.
INCETPC; IPR009065; FERM.
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                                                                                                                   Pfam; PF00373; Band 41; I.
Pfam; PF00595; PDZ; 5.
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1872 187
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2078 207
2233 223
2448 245
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Saras J., Claesson-Welsh L., Heldin C.-H., Gonez L.J.;
"Cloning and Characterization of PTPL1, a protein tyrosine phosphatase
with similarities to cytoskeletal-associated proteins.";
J. Biol. Chem. 269:24082-24089[1994].
                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Protein tyrosine phosphatase, non-receptor type 13 (EC 3.1.3.48)
(Protein-tyrosine phosphatase IB) (PTP-B1) (hPTPE1) (PTP-BAS)
(Protein-tyrosine phosphatase PTPL1) (Res-associated protein-tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maekawa K., Imagawa N., Nagamatsu M., Harada S.;
"Modecular Cloning of a novel protein-tyrosine phosphatase containing
a membrane-binding domain and GLGF repeats.";
FEBS Lett. 337:200-206 (1994).
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 4).

TISSUE=Breast carcinoma;

MEDLINE=94350988; PubMed=8071359;

Banville D., Ahmad S., Stocco R., Shen S.-H.;

"A novel protein-tyrosine phosphatase with homology to both the cytoskeletal proteins of the band 4.1 family and junction-associated guanylate kinases.";

"J. Biol. Chem. 269:22320-22327(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Eye;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sato T., Irie S., Kitada S., Reed J.C.;
"FAP-1: a protein tyrosine phosphatase that associates with Fas.";
Science 268:411-415(1995).
                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
PTND HUMAN STANDARD; PRT; 2485 AA.
Q129<sup>7</sup>3; Q15159; Q15263; Q15264; Q15265; Q15674; Q16826; Q8IWH7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1323-1821 FROM N.A.
Irie S., Hachiya T., Sato T.A.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang H.Y.; Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1279-1883 FROM N.A. (ISOFORM 4). TISSUE=Brain;
                                                                                                                                                                                                         Name=PTPN13; Synonyms=PTP1E, PTPL1, PNP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Leukemia;
MEDLINE=94116679; PubMed=8287977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Fibroblast;
MEDLINE=95014139; PubMed=7929060;
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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Whiting M., Madan A., Ketteman M., Madan A., Rodrigues S., Sanchez A., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.M., Touchman J.W., Green E.D., Dickson M.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Grein J.E., Jones S.J.M., Marra M.A., C-TERMINUS OF TNFRSF6.
MEDLINE=20170882; PubMed=10704206;
Kozlov G., Gehring K., Exiel I.;
"Solution structure of the PDZZ domain from human phosphatase hPTPlE and its interactions with C-terminal peptides from the Fas receptor."; Murthy K.K., Clark K., Fortin Y., Shen S.-H., Banville D.; "ZRP-1, a zyxin-related protein, interacts with the second PDZ domain of the cytosolic protein tyrosine phosphatase hPTP1E."; J. Biol. Chem. 274:20679-20687(1999). INTERACTION WITH NGFR.
MEDLINE=20012928; PubMed=10544233;
Iris = S., Hachiya T., Rabizadeh S., Maruyama W., Mukai J., Li Y.,
Iris e S., Hachiya T., Sabo T.A.;
Reed J.C., Bredesen D.E., Sato T.A.;
"Functional interaction of Fas-associated phosphatase-1 (FAP-1) with STRUCTURE BY NMR OF 1361-1456 IN COMPLEX WITH THE C-TERMINUS OF THE STRUCTURE BY NMR OF 1361-1456 UNCOMPLEXED AND IN COMPLEX WITH THE INTERACTION WITH PLEKHAL AND PLEKHA2.
PubMed=14516276; DOI=10.11042/BJ70031154;
Kimber W.A., Deak M., Prescott A.R., Alessi D.R.;
Kimber W.A., Deak Protein tyrosine phosphatase PTPL1 with the PtdIns(3,4)P2-binding adaptor protein TAPP1.";
Biochem. J. 376:525-535(2003). p75(NTR) and their effect on NF-kappaB activation."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002) INTERACTION WITH TRIP6. MEDLINE=99329089; PubMed=10400701; Biochemistry 39:2572-2580(2000). FEBS Lett. 460:191-198(1999). and mouse cDNA sequences.

GUANINE NUCLEOTIDE EXCHANGE FACTOR RA-GEF-2.
MEDLINE=22090786; PubMed=12095257; DOI=10.1016/S0022-2836(02)00544-2; Kozlov G., Banville D., Gehring K., Ekiel I.; Solution structure of the PDZ2 domain from cytosolic human phosphatase hPTPIE complexed with a peptide reveals contribution of the betaz-beta3 loop to PDZ domain-ligand interactions."; J. Mol. Biol. 320:813-820(2002) MEDLINE=2323362; PubMed=12436199; DOI=10.1007/s100380200094; MEDLINE=2323362; PubMed=12436199; DOI=10.1007/s1003802200094; Yoshida S., Harada H., Fukino K., Teramoto A., Emi M.; Head--to-head juxtaposition of Fas-associated phosphatase-1 (FAP-1) and c-Jun NH2-terminal kinase 3 (ANK3) genes: genomic structure and seven polymorphisms of the FAP-1 gene."; J. Hum. Genet. 47:614-619(2002).
-!- FUNCTION: Regulates negatively FAS-induced apoptosis and NGFR-

tyrosine + phosphate.

SUBUNIT: Interacts with TRIP6 and TNFRSF6 (Fas receptor) through its second PDZ domain. Interacts with the C-terminal SVP motif of NGFR through its third PDZ domain. Interacts with the LIM domain of PDLIM4 through its second and fourth PDZ domains. Binds PLEKHAI and PLEKHAZ through its first PDZ domain.

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

ALTERNATIVE PRODUCTS: mediated pro-apoptotic signaling. CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein

Event=Alternative splicing; Named isoforms=4;

2296 MIWEQKSTVIAMMIQEVEGEKÍKCORÝWPNILGKTIMVSNRLRLALVRMQQLKGFVVRAM 2355

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). MYLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFTVRVF 119 09 1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEBEFYFYIATQGPLPETIEDFWQ 1; Gaps Isoid=012923-4; Sequence=VSP_007921;
Note=May be due to a competing donnor splice site;
INSUE SPECIFICITY: Present in most tissues with the exception of the liver and skeletal muscle. Most abundant in lung, kidney and fetal brain. -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
|-- SIMILARITY: Contains 1 FERM domain.
|-- SIMILARITY: Contains 5 PDZ/DHR domains. Length 2485; GO; GO:0004725; F:protein-tyrosine-phosphatase activity; TAS. GO; GO:000470; P:protein amino acid dephosphorylation; TAS. InterPro: IPR000299; Band 4.1.
InterPro: IPR000265; FERM.
InterPro: IPR011009; Kinase_like.
InterPro: IPR011009; Kinase_like.
InterPro: IPR011036; PH related.
InterPro: IPR000387; TYR_phosphatase.
InterPro: IPR000387; TYR_phosphatase.
InterPro: IPR00037; Tyr_Pp.
Pfam; PF00373; Band 41; I. Indels 46.1%; Score 541.5; DB 1; 47.0%; Pred. No. 1.7e-43; PROSITE; PS50106; PDZ; 5. PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG. 103; Conservative 37; Mismatches IsoId=Q12923-2; Sequence=VSP_000496; IsoId=Q12923-3; Sequence=VSP_000497; IsoId=Q12923-1; Sequence=Displayed; AF233323; AAF63474.1; -. BC039610; AAH39610.1; ALT_TERM. PROSITE; PS00660; FERM 1; FALSE NEG-PROSITE; PS00661; FERM 2; FALSE NEG-Pfam; PF00102; Y phosphatase; 1. PRINTS; PR00935; BAND41. PRINTS; PR00700; PRTYPHPHTASE. EMBL; U12128; AAB60339.1; -.
EMBL; D21209; BAA04750.1; -.
EMBL; D21211; BAA04771.1; -.
EMBL; X80289; CAA55653.1; -.
EMBL; X79676; CAA56124.1; -. FERM_3; 1. PIR; IG7630; I67630.
PDB; 1D5G; NWR; A=1361-1456.
PDB; 1Q7X; NWR; A=1357-1459.
PDB; 3PDZ; NWR; A=1361-1456. L34583; AAC41755.1; Genew; HGNC:9646; PTPN13. PIR; A54971; A54971. PIR; 167629; 167629. Query Match Best Local Similarity PROSITE; PS50057; 600267 Name=3; Name=4 EMBL; EMBL; EMBL; EMBL; Matches MIM; a ਨੇ

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FROM N.A.
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120 QIVKKSTGKSQCVKHLQPTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 VFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVG 177
                                                                                                                                                                                                                                                                                                                                                                                                     MVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQY---FTVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ
                                                                                                                                                                                                                                                                                                                                                                     Gaps
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TISSUB=Oocytes;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                               Length 2500;
                                                                                                                                                                                                                                                                                                                                            46.1%; Score 541.5; DB 2; Length
46.6%; Pred. No. 1.7e-43;
Live 43; Mismatches 70; Indels
                                                                                                                                                                                                                                                                           Lisovsky M.Y., Itoh K., Sokol S.Y.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY327257; AAR97566.1; -.
NON TER 2500 2500
SEQÜENCE 2500 AA; 277694 MW; DODD27366EA19CA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2435 RSGTLICIDVMLALISKDLEFDISNMVHTMRLORHGMIQTE 2475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIGVFICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIQTK 218
                                                      GVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 218
                                                                                                                                                                           Frizzled-8 associated multidomain protein (Fragment)
                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Xenopus laevis (African clawed frog).
                                                                                                                       PRT; 2500 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       920 AA
                                                                                                                                                                                                 Xenopus laevis (African clawed frog)
                                                                                                                                          01-OCT-2004 (TrEMBLrel. 28, 01-OCT-2004 (TrEMBLrel. 28, 01-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                   Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                 Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                             NCBI_TaxID=8355;
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                                                                                                                                                                                       Name=FRIED;
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                                          180
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Bromstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Rack S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
N. Hilalon D.K., Muzny D.W., Sodergen B.M., Gay L.J., Lu X., Gibbs R.A.,
Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 TIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQY 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 FIVRVFQIVKKSTGKSQCVKHLQFIKWPDHGTPASADFFIKYVRYVRKSHITG-PLLVHC 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: Contains I DPZ/DHR domain.
R EMBL; BCO73110; AAH73110.1; -.
R InterPro; IPR000299; Band 4.1.
R InterPro; IPR000799; EZ/rad/moesin.
R InterPro; IPR001478; PDZ.
R InterPro; IPR001478; PDZ.
R InterPro; IPR001399; PTPc—motif.
R InterPro; IPR001399; PTPc—motif.
R InterPro; IPR001399; TYR phosphatase.
R InterPro; IPR00242; TYR PP.
R InterPro; IPR00242; TYR PP.
R FinterPro; IPR00131; Band 41; I.
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SEQUENCE 920 AA, 105109 MW, 8F0BB89C359CD41E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.8%; Score 479; DB 2;
43.6%; Pred. No. 6.9e-38;
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PROSITE; PS00660; FERM 1; UNKNOWN_1.
PROSITE; PS50105; FERM 3; 1.
PROSITE; PS50106; PDZ; 1.
PROSITE; PS60108; TYR PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR PHOSPHATASE_2; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_PTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22341132; PubMed=12454917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fram; PP00103; PD2; I.
Fram; PP00103; Y_phosphatase; 1.
Pram; PR00103; Y_phosphatase; 1.
PRINTS; PR00661; ERMFAMILY.
PRINTS; PR00700; PRTYPHPHTASE.
SWART; SM00228; PB1; 1.
SWART; SM00124; PTPC; 1.
SWART; SM00404; PTPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS;
                                                                                                                                                                                                                                                                                                                                                                               colon."
QYFTVRVFQIVKKSTGKSQCVKHLQFTXMPDHGTPASADFFIKYVRYVRXSHI-TGPLLV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 IAYVSREMLVTNTQTGEEHTVTHLQYVAWPDHGVPDDSSDFLEFVNYVRSLRVDSEPVLV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 QNLDKNRYKDVLPYDTTRVLLQGNEDYINASYVNMEIPAANLVNK-----YIATQGPLPH 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 TIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEH--FSVFLETFHVT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 TCAQFWQVVWDQXLSLIVMLTTLTBRGRTKCHQYWP---DPPDVMNHGGFHIQCQSEDCT 159
790 YVFREMLLIDIETGDEFPIIHLQYVAWPDHGVPDDSSDFLEFATYVRQKRMENQPVLVHC 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ONRDKNRYRDILPYDSTRVPLGKNKDYINASYI-----RIVNHEEEYFYIATQGPLPE
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01-MAY-1992 (Rel. 22, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Protein tyrosine phosphatase, non-receptor type 3 (EC 3.1.3.48)
(Protein-tyrosine phosphatase H1) (PTP-H1).
Name=PTPN3; Synonyms=PTPH1;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                           01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC033716; AA3716.1;

R GO; GO:0016787; F:hydrolase activity; IEA.

R GO; GO:0004702; F:protein the phosphatase activity; IEA.

R GO; GO:0004702; F:protein amino acid dephosphorylation; IEA.

R InterPro; IPR000387; TYR phosphatase.

R InterPro; IPR000242; TYR PP.

R Pfam, PF00102; Y phosphatase.

R PAGNITS; RR00104; PTPC; 1.

R PROSITE; PS00383; TYR PHOSPHATASE.1; 1.

R PROSITE; PS00383; TYR PHOSPHATASE.2; 1.

R PROSITE; PS50055; TYR PHOSPHATASE.2; 1.

R Hydrolase; Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCSAGVGRIGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.3%; Score 468; DB 2; Length 292; 42.3%; Pred. No. 2e-37;
                                                                            78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 AA; 33121 MW; 54B838BDD41D1BD7 CRC64;
                                              173 SAGVGRIGVFICVDVVFSALEKNYSFDIMNIVTOMRKORCGMIOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 913 AA.
                                                                                                                                                                                                      292 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35; Mismatches
                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTN3_HUMAN
P26045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                               phosphatase with homology to the cytoskeletal associated proteins band 4.1, ezrin, and talin.", Proc. Natl. Acad. Sci. U.S.A. 88:5949-5953(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92327504; PubMed=1626183;
Arimura Y., Hinoda Y., Itoh F., Takekawa M., Tsujisaki M., Adachi M.,
Imai K., Yachi A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytoskeleton.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Expression of cytoskeletal-associated protein tyrosine phosphatase PTPH1 mRNA in human hepatocellular carcinoma."; J. Gastroenterol. 29:727-732(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tyrosine + phosphate.
-- SUBCELULAR LOCATION: Cytoplasmic.
--- SIMELARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Imai K., Yachi A.;
"cDNA cloning of new protein tyrosine phosphatases in the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 899-913 FROM N.A.
MEDLINE=9179278; PubMed=7874267;
Ikuta S., Itoh F., Hinoda Y., Toyota M., Makiguchi Y., Imai K.,
Yachi A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM, 176877; -.

GO, GO:0004725; F:protein-tyrosine-phosphatase activity; TAS.
GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000798; Bz/rad/moesin.
InterPro; IPR000798; Bz/rad/moesin.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PP.
PFam; PF00373; Band 41; I.
Pfam; PF00373; Band 41; I.
Pfam; PF00395; PDZ; I.
                                                                                                                                                                                  Yang Q., Tonks N.K.;
"Isolation of a cDNA clone encoding a human protein-tyrosine
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 1 FERM domain.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                    MEDLINE=91296738; PubMed=1648725;
Yang Q., Tonks N.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00102; Y phosphatase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00295; B41; 1.
SMART; SM0028; PD2; 1.
SMART; SM00194; PTPC; 1.
PROSITE; PS00660; FERM 1; 1.
PROSITE; PS00651; FERM 2; 1.
PROSITE; PS50106; PBZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           umour Biol. 13:180-186(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00935; BAND41.
PRINTS; PR00700; PRTYPHPHTASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M64572; AAA35647.1; -. EMBL; S39392; AAB22439.2; -. EMBL; S76309; AAB33583.1; -.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 194-896 FROM N.A.
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MIM; 176877; --
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HSSP; P18031; 1C88.
                                                                                                     SEQUENCE FROM N.A.
                                             NCBI_TaxID=9606;
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Gaps

21;

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54 TIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQ- 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 --YFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVR--KSHITGPL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           789 NPAYIFRKMTLINQEKNESRQLTQIQYTAWPDHGVPDDSSDFLDFVCHVRDQRAGKEEPI 848
                                                                                                                                                                                                                                                                                                                                                                                        1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIR-----IVNHEBEYFYIATQGPLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
Myxinidae; Eptatretinae; Eptatretus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 LVHCSAGVGRTGVFICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIQT 217
                                                                                                                                                                                                                                                                                                                    Query Match 39.3%; Score 461.5; DB 2; Length 926; Best Local Similarity 41.5%; Pred. No. 3.6e-36; Matches 95; Conservative 39; Mismatches 74; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenetics 54:286-291(2002).

EMBL; AB078866; BAC06501.1; -.

GO: 001016787; F:hydrolase activity; IEA.

GO: GO: 00104725; F:protein tyrosine phosphatase activity; IEA.

GO: GO: 0006470; P:protein amino acid dephosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDILINE=22131575; PubMed=12136341;
Nagata T., Suzuki T., Ohta Y., Flajnik M.F., Kasahara M.;
"The leukocyte common antigen (CD45) of the Pacific hagfish, Eptatretus stoutii: implications for the primordial function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               926 AA; 105713 MW; A344DAD4FF7E2AE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation update)
                                                                                                                                   SMART; SM00194; PTPC; 1.

PROSITE; PS00660; FERM 1; UNKNOWN 1.

PROSITE; PS00061; FERM 2; 1.

PROSITE; PS50057; FERM 3; 1.

PROSITE; PS50106; PDZ; 1.

PROSITE; PS60039; TYR PHOSPHATASE 1; 1.

PROSITE; PS50056; TYR PHOSPHATASE 2; 1.

PROSITE; PS50055; TYR PHOSPHATASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003961; FN III.
InterPro; IPR003967; FN III-11ke.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_PP.
Pfam; PF00102; Y_phosphatase; 2.
PRINTS; PR00100; Y_phosphatase; 2.
PRINTS; PR00100; PRTYPHPHTASE.
SWART; SM00109; FN3; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eptatretus stoutii (Pacific hagfish).
               Pfam; PF00595; PDZ; 1.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00935; BAND41.
PRINTS; PR00661; ERMFAMILY.
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00295; B41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD45 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=PTPRC;
                                                                                                                                                                                                                                                                        Hydrolase.
                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD45.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
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                                                                                                                                                                                                                                                                                      54 TIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEH--FSVFLETFHVT 111
                                                                                                                                                                                                                                                                                                                                                                                                    112 OYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHI-TGPLLV 170
                                                                                                                                                                                                                                                                   1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYI------RIVNHEEBYFYIATQGPLPE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ., IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Testis;
MEDIATE=20510023; PubMed=11054567;
ARELINE=20510023; PubMed=11054567;
Park K.W., Lee E.J., Lee S.H., Lee J.E., Choi E.Y., Kim B.J.,
Hwang R., Park K.A., Baik J.H.;
"Molecular cloning and characterization of a protein tyrosine
phosphatase enriched in testis, a putative murine homologue of human
                                                                                                                                                                                                                                       18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
NCBI_TaxID=10090;
PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
Cytoskeleton; Hydrolase; Protein_Phosphatase; Structural protein.
29 312 FERM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Testis;
Choi E.-Y., Park K.-W., Lee E.-J., Baik J.-H.;
Choi E.-Y., Park K.-W., Lee E.-J., Baik J.-H.;
Choi E.-Y., Park K.-W., Lee E.-J., Baik J.-H.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
EMBL; AF106702; AAD22773.1; -.
HSSP; P1171; 1GG3.
HSSP; P1171; 1GG3.
HSSP; P1171; 1GG3.
GO; GO:0004726; Ptpn4.
GO; GO:0004726; F:non-membrane spanning protein tyrosine phos.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000998; Ezyrad/moesin.
                                                                                                                   Protein-tyrosine phosphatase.
Phosphocysteine intermediate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.8%; Score 467; DB 1; Length 913; 42.3%; Pred. No. 1e-36; ative 35; Mismatches 78; Indels
                                                                                                                                                                    29A539ACDE2F1515 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Testis-enriched protein tyrosine phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            926 AA
                                                                                                                                                      similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001478; PDZ.
InterPro; IPR011036; PH related.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_PP.
Pfam; PF00373; Band_41; T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                    913 AA; 104029 MW;
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                                                                                                                                                                                                                                 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                   842
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                                                                                                                                                                                                                   Similarity
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                                                                                                510
670
842
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                                                                                                                                                                  SEQUENCE
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                                                                                                                                   ACT_SITE
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Best Local
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57 DFWOMVLENNCNVIAMITREIECGVIKCYSYMPISLKEPLEFEHFSVFLETFHVTQYFTV 116
                                                                                                                           496 NNGKNRYSDILPYDNNRVRLVSNGGKPGSDYINASYIN--GYKESKKYICAQGPMEETAA 553
                                                                                                                                                                                                                                                                                                                                                    612 IITKISLNHGGNSRIITHVQFTKWPDHGVPDDPDLLLRLRRRVLSFCNFFDGPMVVHCSA
                                                                          2 NRDKNRYRDILPYDSTRVPLGKN-----KDYINASYIRIVNHEEEYFYIATQGPLPETIE
                                                                                                                                                                                                                                         554 EFWTMIWEQKTAVIIMVTRCIBGGKNKCYQYWPRQKGKKLEFKSLSV--TNNEVMLYPDX
                                                                                                                                                                                                                                                                                                   117 RVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRK--SHITGPLLVHCSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eptatretus stoutii (Pacific hagfish).
Bukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniformes;
Myxinidae; Eptatretinae; Eptatretus.
NCBI_TaxID=7765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
42.9%; Pred. No. 3.4e-35; ive 28; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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22,
26,
                               96; Conservative
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01-OCT-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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     Similarity
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     Best Local
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                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              678 EFWIMIWEQKTAVIIMVTRCIEGGKNKCYQYWPRQKGKKLEFKSLSV--TNNEVMLYPDY 735
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                                                                                                                                                                                                                                                                                                                                        2 NRDKNRYRDILPYDSTRVPLGKN-----KDYINASYIRIVNHEEEYFYIATQGPLPETIE
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Eukaryota, Metazoa, Chordata, Craniata, Hyperotreti, Myxiniformes,
Myxinidae, Eptatretinae, Eptatretus.
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                                                                                                                                                                                                                           38.6%; Score 453.5; DB 2; Length 1222; 42.9%; Pred. No. 3.1e-35; arive 28; Mismatches 89; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22131575; PubMed=12136341;
Nagata T., Suzuki T., Ohta Y., Flajnik M.F., Kasahara M.;
"The leukocyte common antigen (CD45) of the Pacific hagfish,
Epterretus stoutii: implications for the primordial function
CD45.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenetics 54:286-291(2002).

EMBL; AB078865; BAC06500.1; -.

GO: 001016787; F:hydrolase activity; IEA.

GO: GO: 00104725; F:protein tyrosine phosphatase activity; IEA.

GO: GO: 0006470; P:protein amino acid dephosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1222 AA; 137895 MW; 1A3965AA3E6B4E69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003961; FN III aminio acid depud InterPro; IPR003961; FN III.
InterPro; IPR003967; FN III.-like.
InterPro; IPR000347; TYR_phosphatase.
Pfam; PF00041; fn3; 3.
Pfam; PF00041; FN PP.
Pram; PF00102; Y_phosphatase; 2.
PR01175; PR00100; PRTYPHPHTASE.
SMART; SM00104; PTPC; 2.
PROSITE; PS50853; FN3; 2.
PROSITE; PS50833; TYR_PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE 2; 2.
PROSITE; PS50056; TYR_PHOSPHATASE 2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 452.5;
           PROSITE; PS50853; FN3; 2.
PROSITE; PS00831; TYR PHOSPHATASE 1; 2.
PROSITE; PS50056; TYR PHOSPHATASE 2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP;
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                                                                                                                                                                                                                                                                                          96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Gaps
                                                                                                                                                EMBL, AB078868; BAC06503.1; --
R GO, GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:000470; F:hydrolase activity; IEA.
GO; GO:000470; P:protein tyrosine phosphatase activity; IEA.
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
R InterPro; IPR0003861; FW III.
R InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
R InterPro; IPR00041; fm3; 3.
Fpam; PF00041; fm3; 3.
Fpam; PF000041; FMYPHPHTASE.
R PRINTS; PR00100; PRTYPHPHTASE.
R RART; SM00100; FN3; 2.
R RART; SM01096; FN3; 2.
R RRSTIE; PS00853; FN3; 2.
R RRSTIE; PS0085; TYR_PHOSPHATASE_1; 2.
R PROSITE; PS0086; TYR_PHOSPHATASE_2; 2.
R PROSITE; PS0085; TYR_PHOSPHATASE_2; 2.
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MEDLINE=22131575; PubMed=12136341;
Nagata T., Suzuki T., Ohta Y., Flajnik M.F., Kasahara M.;
"The leukocyte common antigen (CD45) of the Pacific hagfish,
Eptatretus stoutii: implications for the primordial function
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Hydrolase.
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                                               RESULT 15
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643 EFWIMIWEQKTAVIIMVTRCIEGGKNKCYQYWPRQKGKKLEFKSLSV--INNEVMLYPDY 700
                                                                                     117 RVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRK--SHITGPLLVHCSA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600 NNGKNRYSDILPYDNNRVRLVSNGGKPGSDYINASYIN--GYKESKKYICAQGPMEETAA 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 RVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRK--SHITGPLLVHCSA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NRDKNRYRDILPYDSTRVPLGKN-----KDYINASYIRIVNHEEBYFYIATQGPLPETIE 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eptatretus stoutii (Pacific hagfish).
Eukaryota, Metazoa; Chordata, Craniata, Hyperotreti; Myxiniformes;
Myxinidae; Eptatretinae; Eptatretus.
NCBI_TaxID=7765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=22131575; PubMed=12136341;
Nagata T., Suzuki T., Ohta Y., Flajnik M.F., Kasahara M.;
The leukocyte common antigen (CD45) of the Pacific hagfish,
Eptatretus stoutii: implications for the primordial function
CD45.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB078867; BAC06502.1; -...
GO: 0016787; F:hydrolase activity; IEA.
GO: 001004725; F:protein tyrosine phosphatase activity; IEA.
GO: 00006470; P:protein amino acid dephosphorylation; IEA.
InterPro: IPR003951; FW III.
InterPro: IPR003957; FW_III-like.
InterPro: IPR003957; TW_FIII-like.
InterPro: IPR002421; TYR_PP.
                                                                                                                                                                                                                                                                                                                                    GVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8MY43;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
CD45 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1202 AA
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PROSITE; PS00383; TYR PHOSPHATASE 1; 2.
PROSITE; PS50056; TYR PHOSPHATASE 2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00102; Y_phosphatase; 2. PRINTS; PR00700; PRIYPPHTASE. SMART; SM0060; FN3; 3. SMART; SM00194; PTPC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenetics 54:286-291(2002).
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                            MEDINE-22220060; PubMed=12234928;

Nawroth R., Poell G., Ranft A., Kloep S., Samulowitz U., Fachinger G., Golding M., Shima D.T., Deutsch U., Vestweber D.;

"VE-PTP and VE-cadherin ectodomains interact to facilitate regulation of phosphorylation and cell contacts.";

EMBO J. 21:4885-4895(2020)

EMBL, AV077755, AAL78813.1;

HSSP; P18052, 1YFO.

GO, GO:0016775; F.hydrolase activity, IEA.

GO, GO:0016725; F.protein phosphorylation; IEA.

GO, GO:0006470; P.protein amino acid dephosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDFWKMAWEQNVHIIVMVTQCVEXGRVKCDHYWPAD-QDPLYYGDLILQMVSESVLPEWT
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                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1998 AA; 224474 MW; B37EA6501EF03E5D CRC64;
                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                 Vascular endothelial protein tyrosine phosphatase.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.3%; Score 449.5; DB 2; 41.2%; Pred. No. 1.4e-34; ive 40; Mismatches 81;
1998 AA
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PROSITE; PS60383; TYR PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR PHOSPHATASE_PTP; 1.
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InterPro; IPR008957; FN_III-11ke.
InterPro; IPR008957; TY_Dhosphatase.
InterPro; IPR000242; TY_P.P.
Pfam; PF00102; Tyhosphatase; 1.
PkINYS; PR00100; Y_Dhosphatase; 1.
PRINYS; PR00100; PRYPHPHTASE.
                                                             Created)
   PRT;
                                                                                      01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity 41.2%
PRELIMINARY;
                                                          01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=Swiss Webster;
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                  Copyright
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OM protein - protein search, using sw model

Run on:

December 1, 2004, 12:07:42 ; Search time 18.4854 Seconds (without alignments) 1134.694 Million cell updates/sec

US-09-095-478A-7_COPY_188_405 1174 1 QNRDKNRYRDILPYDSTRVP......DIMNIVTQMRKQRCGMIQTK 218 Title: Perfect score: Sequence:

283416 seqs, 96216763 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: Dir1:*
2: Dir2:*
3: Dir3:*
4: Dir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	SUMMARIES	Description	16	in-tvrosi	protein-tvros	protein-	protein-tvrosine	protein-tyrosine	protein-tyrosin	protein-				protein-tyrosine	S68700 HPTP beta-like tvr							613 protein-tyrosine-p			protein-	protein-	50 protein-tyrosine-n	1 protein-tyrosine	8 protein-tvrosine	protein-tvros	outroot for utonotal
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Ouery Core Match Length 41.5 46.6 22594 41.5 46.1 22684 44.4 33.5 45.4 2490 33.5 45.4 37.9 1997 43.5 37.9 32.5 36.4 11076 27.5 36.4 11076 27.5 36.4 11076 25.5 36.2 1496		Result No.	1	7	æ	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	ć

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protein-tyrosine-phosphatase (BC 3.1.3.48), nonreceptor type 13 - mouse
NyAlternate names: epidernal growth factor-binding protein; serine proteinase
C;Species: Was musculus (house mouse)
C;Species: Mas musculus (house mouse)
C;Accession: S71625; S67987; I81210; I81209; S40290
E;Chda, D.; Kume, T.; Mukouyama, Y.; Tabata, S.; Nomura, N.; Thomas, M.L.; Watanabe, PBS Lett. 358, 233-239, 1995
A;Title: Characterization of a protein tyrosine phosphatase (RIP) expressed at a very excession: S71625; MUID:95145716; PMID:7843407
A;Molecule type: mRNA

RESULT 2 S71625

protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-n	protein-tyrosine-p	leukocyte common a	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p							
JW0049	TODULT	JC7503	817669	I38140	S17670	B53978	A53978	150212	S51005	A28334	A46546	TPHUNI	JC2366	A46151
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356	1273	1226	1452	1174	1452	597	694	1499	1175	1291	1304	435	1189	2314
36.2	36.1	36.0	36.0	36.0	35.9	35.9	35.9	35.8	35.7	35.7	35.7	35.6	35.4	35.4
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425	424	4.2	423	422.5	4	7.	•	•	41	4.	4	4	4	415.5

ALIGNMENTS

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C;Accession: 167629
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FEBS Lett. 376, 177-180, 1955
A;Title: Righdermal growth factor-binding protein activates soluble and receptor-bound singletes and under: S67987; MUDD:96108375; PMID:7498536
A;Reference number: S67987; MUDD:96108375; PMID:7498536
A;Reference number: S67987
A;Residues: 1038-1102 *MOL>
A;Experimental source: submaxillary glands
A;Accession: 181210
A;Accession: 181210
A;Accession: 181209
A;Accession: 181209
A;Cross-references: GB:134582; NID:9806297; PIDN:AAC42056.1; PID:9806296
A;Cross-references: GB:134581; NID:9806295; PIDN:AAC42055.1; PID:9806296
A;Accession: 181209
A;Accession: 181209
A;Accession: C; Zeeuwen, P.; Schepens, J.; Wieringa, B.
B;Bendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
B;Bendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
A;Reference number: S40280
A;Accession: Status number: S40280
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C. Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
C. Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
C. Keywords: phosphortein; phosphoric monoester hydrolase; transmembrane protein; tyros
F; Se6-860/Domain: protein 4.1 membrane-binding domain homology < GLG1>
F; 1089-1165/Domain: GLGF domain homology < GLG2>
F; 1361-1437/Domain: GLGF domain homology < GLG3>
F; 1495-1574/Domain: GLGF domain homology < GLG3>
F; 1863-1937/Domain: GLGF domain homology < GLG5>
F; 1863-1937/Domain: GLGF domain homolo
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A;Residues: 1-2450 <CHI>
A;Cross-references: UNIPROT:Q64512; UNIPROT:Q62370; EMBL:D83966; NID:g1232103; PIDN:BAA1
A;Experimental source: strain DBA/2; cell line MEL 745A
R;Wolf, B.B.: Brown. M D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the expression levels of murine protein-tyrosine phosphatas
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A;Residues: 2266-2372 <HEN>
A;Cross-references: EMBL:Z23059; NID:g438155; PIDN:CAA80594.1; PID:g438156
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F)1769-1841937/Domain: GLGF domain homology <GLG5>
F)2203-2422/Domain: protein-tyrosine-phosphatase homology <PTP1>
F)2314/Active site: Cys (phosphocysteine intermediate) #status predicted
F)2380/Binding site: substrate phosphate (Arg) #status predicted
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ilarity 49.1%; Pred. No. 1.1e-42;
Conservative 35; Mismatches 71;
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I67630
R;Mackawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
R;Mackawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
A;EBS Lett. 337, 200-206, 1994
A;Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane
A;Reference number: I53483; MUID:94116679; PMID:8287977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-2294 «RES»
A; Residues: 1-2294 «RES»
A; Cross-references: UNINROT:Q12923; GB:D21211; NID:g452193; PIDN:BAA04752.1; PID:g452194
A; Cross-references: UNINROT:Q12923; GB:D21211; NID:g452193; GIGF domain homology;
C; Superfamily: protein-tyrosine-phosphatase
C; Keywords: phosphoric monoester hydrolase
C; Keywords: phosphoric monoester hydrolase
F; 574-868 Domain: protein 4.1 membrane-binding domain homology «B41»
F; 71486-1258 Domain: gidF domain homology «CG2»
F; 2046-2265 Domain: protein-tyrosine-phosphatase homology «PTP»
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Figh ackaus, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
Figh ackaus, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
Figh ackaus Lett. 377, 200-206, 1994
A;Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membran A;Reference number: I53483; MUID:94116679; PMID:8287977
A;Reference number: I5529
A;Residue: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule t
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QNRDKONRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEFYFYIATQGPLPETIEDFWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 QIVKKSIGKSQCVKHLOFIKWPDHGTPASADFFIKYVRYVRKSHIIGPLLVHCSAGVGRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEBYFYIATQGPLPETIEDFWQ
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46.1%; Score 541.5; DB 2;
Best Local Similarity 47.0%; Pred. No. 3.9e-42;
Matches 103; Conservative 37; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK
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Pred. No. 3.6e-42;
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Best Local Similarity 47.0%;
Matches 103; Conservative 3
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A;Accession: A41109
A;Molecule type: mRNA
A;Residues: 1-913 <72NA>
A;Molecule type: mRNA
A;Cross-references: UNIPROT: P26045; GB:M64572; NID:9179912; PIDN:AAA35647.1; PID:9179913
A;Cross-references: UNIPROT: P26045; GB:M64572; NID:9179912; PIDN:AAA35647.1; PID:9179913
A;Cross-references: UNIPROT: P26045; GB:M64572; NID:9179912; PIDN:AAA35647.1; PID:9179913
A;Cross-reference: Topoda, Y:; Toyota, M.; Makiguchi, Y:; Imai, K.; Yachi, A.
A;Title: Expression of cytoskeletal-associated protein tyrosine phosphatase PTPH1 mRNA i A;Reference number: I55698, MID:95179278; PMID:7874267
A;Accession: I55698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.Yang, Q.; Tonks, N.K.
Proc. Natl. Acad. Sci. U.S.A. 88, 5949-5953, 1991
A;Title: Isolation of a cDNA clone encoding a human protein-tyrosine phosphatase with
A;Reference number: A41109; MUID:91296738; PMID:1648725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                          protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN3, nonreceptor type 3 [validated] N.Alternate names: PTPH1 (S.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: 27-Mar-1992 #sequence_revision 02-May-1994 #text_change 09-Jul-2004 C.Accession: A41109: 155698
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61 MVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFTVRVF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         669 ONLDKNRYKDVLPYDTTRVLLQGNEDYINASYVNMEIPAANLVNK-----YIATQGPLPH 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:S76309; NID:g913165; PIDN:AAB33583.1; PID:g913166 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;842/Active site: Cys (phosphocysteine intermediate) #status predicted
F;848/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 HCSAGVGRIGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 913;
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39.8%; Score 467; DB 1; Length 31
Best Local Similarity 42.3%; Pred. No. 1.2e-35;
Matches 96; Conservative 35; Mismatches 78; Indels
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A; Residues: 899-913 < RES>
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A,Residues: 1-61, GS', G-839, D', 841-1055,1075-1133, FH',1136-1210, I',1212-1383,1389-15

A,Cross-references: GB:X80289; NID:9515030; PIDN:CAA56563.1; PID:9515031

R,Sato, T.; Irie, S.; Kitada, S.; Reed, J.C.

R,Sato, T.; Irie, S.; Kitada, S.; Reed, J.C.

A,Title: FAP-1: a protein tyrosine phosphatase that associates with Fas.

A,Reference number: 159595; MUID:95232528; PMID:7536343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: sequence shown follows authors' translation at positions 62-63
R;Saras, J.; Claesson-Welsh, L.; Heldin, C.H.; Gonez, L.J.
D biol. Chem. 269, 24082-24089, 1994
A;Title: Cloning and characterization of PTPLI, a protein tyrosine phosphatase with simi
A;Reference number: A55114; MUID:95014139; PMID:7929060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
FEBS Lett. 337, 200-206, 1994
A;Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane
A;Reference number: IS3483; MUID:94116679; PMID:8287977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prd
                                                                                                                                                                                                                                                             protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 1 [v
N;Alternate names: Fas-associated phosphatase FAP-1; protein-tyrosine-phosphatase hPTP1F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Title: A novel protein-tyrosine phosphatase with homology to both the cytoskeletal A,Reference number: A54971; MUID:94350988; PMID:8071359
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      TLEDIOTREVRHISHLNFTAWPDHDTPSOPDDLLTFISYMRHIHRSGPIITHCSAGIGRS 2396
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R;Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
FEBS Lett. 337, 200-206, 1994
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Cys (phosphocysteine intermediate) #status pi
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; Pred. No. 2.2e-41;
39; Mismatches 78;
                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 11-Nov-1994 #sequence revision 08-Feb-1996 #
C;Accession: A54971; A55144; I59595; IS3483; S46955
R;Banville, D.; Ahmad, S.; Stocco, R.; Shen, S.H.
J. Biol. Chem. 269, 22320-22327, 1994
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A,Molecule type: mRN
Residues: 1-2490 «BAN»
A,Cross-references: UNIPROT:Q12923; GB:U12128
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1279-1888 <RES>
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Best Local Similarity 46.1%
Matches 101; Conservative
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2413/Active site:
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C. Superfamily: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III re C. Superfamily: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III re C. Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; recept F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-1692/Porduct: protein-tyrosine-phosphatase, receptor type beta #status predicted <MT>
F;23-1652/Domain: extracellular #status predicted <SIT>
F;1626-1642/Domain: intracellular #status predicted <ITM>
F;163-1997/Domain: intracellular #status predicted <ITM>
F;1727-1952/Domain: protein-tyrosine-phosphatase homology <PTP>
F;1904/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1910/Binding site: substrate phosphate (Arg) #status predicted
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A,Experimental source: megakaryocytes, cell line MEG-10
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C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; p
C; Reywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
F; 31-308/Domain: protein 4.1 membrane-binding domain homology < B41>
F; 523-597/Domain: GLGF domain homology < GLG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1726 ENRGKNRYNNILPYDATRVKLSNVDDDPCSDYINASYIPGNNFRRE--YIVTQGPLPGTK 1783
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R;Gu, M.; York, J.D.; Warshawsky, I.; Majerus, P.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 5867-5871, 1991
A;Title: Identification, cloning, and expression of a cytosolic megakaryocyte;
A;Reference number: A41105; WUID:91288564; PMID:1648233
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C,Date: 20-Mar-1992 #sequence_revision 02-May-1994 #text_change 09-Jul-2004
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F;852/Active site: Cys (phosphocysteine intermediate) #status predicted
F;858/Binding site: substrate phosphate (Arg) #status predicted
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llarity 41.0%; Pred. No. 1.6e-33;
Conservative 35; Mismatches 79;
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                                                                                                                            A, Cross-references: GDB:127352; OMIM:176882
A, Map position: 12q15-12q21
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N,Alternate names: PTPase MEG
A; Residues: 1872-1997 < VR2>
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Matches 94; Conserv
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A; Residues: 1-926 <GUA>
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                                                 C; Genetics:
A; Gene: GDB: PTPRB;
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                             C; Specias: Mus musculus (notes mouse)
C; Specias: Mus musculus (notes mouse)
C; Date: 22-Nov-1993 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004
C; Accession: 817671; 840287
C; Accession: 817671; 840287
C; Accession: 817671; 840287
R; Gebbint, M. R. B. G.; Van Etten, I.; Hateboer, G.; Suijkerbuijk, R.; Beijersbergen, R.L.; FBSS Lett. 290, 123-130, 1991
A; Reference number: 517669; MUID: 92008644; PMID: 1655529
A; Accession: 81767
A; Accession: 817689; MUID: 92008644; PMID: 1655529
A; Accession: 817689; MUID: 92008644; PMID: 1655529
A; Accession: 817689; MUID: 92008644; PMID: 1655529
A; Residues: 1-583 cGBB>
A; Residues: 1-583 cGBB>
A; Cross-references: UNIPROT: Q64497; EMBL: X58289
R; Hendriks, W.; Brugaman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
Submitted to the EMBL Data Library, June 1993
A; Rescription: Assessment of the expression levels of murine protein-tyrosine phosphatas
A; Rescription: Assessment of the expression levels of murine protein-tyrosine phosphatase, receptor type beta; fibronectin type III re
C; Superfamily: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III re
C; Keywords: phosphorotein: phosphoroteine intermediate) #status predicted
F; 311-536/Domain: protein-tyrosine-phosphate (Arg) #status predicted
F; 494/Binding site: substrate phosphate (Arg) #status predicted
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A,Accession: $12050
A,Accession: $12050
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-1997 < KRN
B,Residues: 1-1997 < KRN
A,Cross-references: UNIPROT:P23467; GB.X54131; NID:g35787; PIDN:CAA38066.1; PID:g35788
R;de Vries, L.; Li, R.Y.; Ragab, A.; Ragab-Thomas, J.M.F.; Chap, H.
A,Title: Expression of a truncated protein-tyrosine phosphatase mRNA in human lung.
A,Reference number: $15818; MUID:91243813; PMID:1645282
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C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S12050; S15818; $15819
R;Krueger, N.X.; Streuli, M.; Saito, H.
EMBO J. 9, 3241-3252, 1990
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Best Local Similarity 41.2%; Pred. No. 3.8e-34;
Matches 94; Conservative 40; Mismatches 81
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A; Residues: 1872-1911, 'VHMVLQK' <VRI>
              C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
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C; Accession: T30938
R; Gershon, T.R.; Baker, M.; Nitabach, M.; Wu, P.; Macagno, E.R.
submitted to the EMBL Data Library, December 1997
A; Description: Two receptor tyrosine phosphatases of the LaR subfamily are expressed in A; Reference number: 220939
A; Accession: T30938
A; Accession: T30938
A; Accession: T30938
A; Accession: Lype: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: MRNA
A; Cross-references: UNIPROT: 044328; EMBL: AF017083; NID: 92695654; PID: 92695655; PIDN: AABB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Accession: A38191
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-382 <MOS>
A.Cross-references: UNIPROT:Q06180; GB:M81477; NID:g192683; PIDN:AAA37446.1; PID:g192684
A.Note: sequence extracted from NCBI backbone (NCBIN:75809, NCBIP:75812)
C.Comment: This transcript was found in a variety of embryonic and adult trissues. A shot c. Superfamily: protein-tyrosine-phosphatase, nonreceptor type 1; protein-tyrosine-phosphoryctein: phosphoric monoester hydrolase; tyrosi C.Keywords: alternative splicing; phosphatase homology <PTP>
F.22/Abomain: protein-tyrosine-phosphatase homology <PTP>
F.22/Abunding site: substrate phosphate (Arg) #status predicted
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C.Species: Mus musculus (house mouse)
C.Date: 17-Feb-1994 #sequence_revision 02-May-1994 #text_change 09-Jul-2004
C.Accession: A33191
R.Mosinger Jr., B.; Tillmann, U.; Westphal, H.; Tremblay, M.L.
R.Mosinger Jr., B.; Tillmann, U.S.A. 38, 499-503, 1992
A.Title: Cloning and characterization of a mouse cDNA encoding a cytoplasmic protein-tyz A;Reference number: A38191; MUID:92115688; PMID:1731319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene: LAR2
Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSH----ITGPLLVH 171
                                             RVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKY---VR-YVRKSHITGPLLVHC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor tyrosine phosphatase - medicinal leech
C;Species: Hirudo medicinalis (medicinal leech)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 NRDKNRYRDILPYDSTRVPLG----KNKDYINASYIRIVNHEEEYFYIATQGPLPETIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 39.65
Matches 90; Conservative
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C/Goment: Enhanced expression of this protein with increasing cell density suggests a r C/Genetics:
A/Gene: GDB:PTPRJ
A/Cross-references: GDB:385040, OMIM:600925
A/Map position: 19q13.4-19q13.4
C/FUNCTION:
A/Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and C/Bymortion: adaptaces hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and C/Bymortion: asymptocently phosphotrein; phosphortein; phosphortein; phosphortein; phosphortein; phosphortein; phosphortein proportion and F:1-35/Domain: signal sequence #status predicted <SIGNS-F:1-35/Domain: signal sequence #status predicted <SIGNS-F:135/Domain: fibronectin type III repeat homology astNas-F:284-356/Domain: fibronectin type III repeat homology #status atypical <3FNCS-F:365-445/Domain: fibronectin type III repeat homology astNas-F:365-445/Domain: fibronectin type III repeat homology astNas-F:360-804/Domain: fibronec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           procein-tyrosine-phosphatase (EC 3.1.3.48), receptor type J precursor - human NyAlternate names: density enhanced phosphatase-1 (DEP-1); protein-tyrosine phosphatase (Species: Homo sapiens (man) (Species: Homo sapiens (mar-1996 #sequence_revision 08-Mar-1996 #text_change 09-Jul-2004 (Speciesion: 138670; 12.559) (Multiple: Mar-1996 #text_change 09-Jul-2004 (Speciesion: 138670; U.S.A. 91, 9680-9684, 1994 (Multiple: Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is enhanced A; Reference number: 138670; Multiple: Multip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;1065-1287/Domain: protein-tyrosine-phosphatase homology <PTP>
F;12,82,93,3104,142,172,1292,231,258,278,342,351,376,391,365,313,361,525,536,582,603,
F;1229/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1245/Binding site: substrate phosphate (Arg) #status predicted
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                                                                                          ---EPTGSSSYGCYQVTCHSEEG 788
                                                                                                                                                                                114 FTVRVFQ---IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHI--TGPL 168
                                                                                                                                                                                                                                                                           789 NTAYIFRKMTLFNQEKNESRPLTQIQYIAWPDHGVPDDSSDFLDFVCHVRNKRAGKEEPV 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTV 116
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TIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQY
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                                                                                                                                                                                                                                                                                                                                                                                      LVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                        37.8%; Score 444; DB 1; Length 1337; 41.2%; Pred. No. 2.7e-33;
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A;Molecule type: mRNA
                                                       42; Mismatches
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R;Champion-Arnaud, P.; Gesnel, M.C.; Foulkes, N.; Ronsin, C.; Sassone-Corsi, P.; Breathn Oncogene 6, 1203-1209, 1991
A;Tile: Activation of transcription via AP-1 or CREB regulatory sites is blocked by pro A;Reference number: A60345; MUID:91319401; PMID:1650442
A;Accession: A60345
                                                                                                                                                                                                                                                                                                                                                     A/Gene: GDB:PTPN2; PTPT
A/Gene: GDB:PTPN2; PTPT
A/Cross-references: GDB:128098; OMIM:176887
A/Cross-references: GDB:128098; OMIM:176887
A/Cross-references: GDB:122-18p11.21
A/Introns: 347/2; 381/2
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 1; protein-tyrosine-phosphorocine; phosphoric monoester hydrolase; tyrosi F;42-264/Domain: protein-tyrosine-phosphatase homology <PTP>F;42-264/Domain: protein-tyrosine-phosphatese homology <PTP>F;216/Active site: Cys (phosphoryeteine intermediate) #status predicted
F;222/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 QMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFE-HFSVFLETFHVTQYFTVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QNRDKNRYRDILPYDSTRVPL-GKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 FQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAGVGRIGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 435; DB 1;
Pred, No. 4.3e-33;
                                                                                                                                                                                                                                               A;Status: not compared with conceptual translation A;Molecule type: DNA A;Residues: 348-387 <CH2>
                                                                                                                                                    A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.9%;
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A; Accession: S21831
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A;Molecule type: mRNA
A;Residues: 1-363 <SWA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-387 < CHA>
                                                                                                                                                                                                                                A; Accession: B60345
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A, Status: preliminary; nucleic acid sequence not shown
A, Status: preliminary; nucleic acid sequence not shown
A, Molecule type: mRNA
A, Molecule: 1-1238 «KUR»
A, Gressidues: 1-1238 «KUR»
A, Gressidues: 1-1238 «KUR»
A, Greetics:
C, Genetics:
A, Map position: 2E1-2
C, Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III repeat
C, Superfamily: protein-tyrosine-phosphatase #status predicted <SIG>C, Superfamily: protein-tyrosine-phosphatase #status predicted <MAT>
F, 29 (Domain: signal sequence #status phosphatase #status predicted <MAT>
F, 29 (Domain: protein-tyrosine-phosphatase homology <3FR>
F, 267-347/Domain: protein-tyrosine-phosphatase homology <PTP>
F, 218 (Phosphosphatase homology <ATP>
F, 2146/Dative site: Cys (phosphosphatase homology <PTP>
F, 1146/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a murine receptor-type tyrosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 RVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHI-----TGPLLVH 171
                                                                                                                                                                                                              118
                                                                                                                                                                                                                                             |: :||::: | :|||| | | | | ::: ||:|
159 LQLENINTGETRIISHFHYTTWPDFGVPESPASFLNFLFKVRESGCLTPDHGPAVIHCSA 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ONRDKNRYRDILPYDSTRVPLG----KNKDYINASYIRIVNHEEEYFYIATQGPLPETIE 56
                                                                                                             59
                                                                                                                                                            98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004 C;Accession: S68700 C;Accession: S.; Matsuda, Y.; Saitoh, T.; Ohsugi, M.; Yamamoto, S;Kuramochi, S.; Matsuda, Y.; Saitoh, T.; Ohsugi, M.; Yamamoto, FBBS Lett. 378, 7-14, 1996 A;Title: Molecular cloning and characterization of Byp, a murine receptor-typ A;Reference number: S68700; MUID:96140699; PMID:8549806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
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                                                                                                             1 ONRDKNRYRDILPYDSTRVPL-GKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFW
                                                                                                                                                         41 ENRNRNRYRDVSPYDHSRVKLQSTENDYINASLVDI--EEAQRSYILTQGPLPNTCCHFW
                                                           Gaps
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                                                                                                                                                                                                                                                                                                                 119 FQIVKKSIGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHIT----
               Length 382;
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 GVGRIGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 436; DB 1; Lc
Pred. No. 3.4e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPTP beta-like tyrosine phosphatase precursor - mouse C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.1%; Score 436; DB 2; 39.6%; Pred. No. 1.4e-32;
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                                                                 38; Mismatches
                                         40.48;
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                                                                 90; Conservative
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Best Local Similarity
Matches 90; Conserv
               Query Match
Best Local Similarity
Matches 90; Conserv
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R;Swarup, G.; Kamatkar, S.; Radha, V.; Rema, V. FEBS Lett. 280, 65-69, 1991
A,Title: Molecular cloning and expression of a protein-tyrosine phosphatase showing home A,Reference number: S14294; MUID:91184422; PMID:1849097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X58828; NID:G56995; PIDN:CAA41633.1; PID:G56996
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 1; protein-tyrosine-phosp
C;Keywords: alternative splicing; DNA binding; phosphototein; phosphoric monoester hyd
F;42-264/Domain: protein-tyrosine-phosphatase homology <PTP>
F;216/Active site: Cys (phosphocysteine intermediate) #status predicted
F;222/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                            protein-tyrosine-phosphatase (EC 3.1.3.48) 11A - rat
C.Species: Rattus norvegicus (Norway rat)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C.Accession: S14294; S21831
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protein-tyrosine-phosphatase (BC 3.1.3.48) 11A - human C;Species: Homo sapiens (man) C;Date: 20-Feb-1993 #sequence_revision 02-May-1994 #text_change 24-Apr-1998

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60 OMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFE-HFSVFLETFHVTQYFTVRV 118
                                Query Match 37.0%; Score 414; DB 1; Length 363;
Best Local Similarity 40.4%; Pred. No. 5e-33;
Matches 91; Conservative 38; Mismatches 84; Indels 12; Gaps
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Search completed: December 1, 2004, 12:17:28 Job time : 18.4854 secs

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14
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19: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1582122 segs, 356623098 residues
                                                                                                                                                                                                                                                                                                                                                            US-09-095-478A-7_COPY_188_405
1174
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Maximum Match 1008
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                                       - protein search,
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Appli	Appl	Appl	Appl									
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Description	Sequence	Sequence	Sequence										
SUMMARIES	US-09-095-478-6	US-09-095-478-8	US-09-095-478-3	US-09-095-478-1	US-09-095-478-2	US-10-311-764-4	US-09-095-478-4	US-09-095-478-5	US-09-095-478-7	US-09-095-478-9	US-10-060-065-35	US-10-059-585-56	US-10-177-980-12
	10	10	10	10	10	15	10	10	10	10	14	14	14
% Query Match Length DB	354	379	412	426	463	420	122	122	381	358	1267	1267	2466
% Query Match	100.0	100.0	100.0	100.0	100.0	79.7	56.9	48.2	46.9	46.1	46.1	46.1	46.1
Score	1174	1174	1174	1174	1174	936	668	266	550.5	541.5	541.5	541.5	541.5
Result No.	П	73	m	4	2	9	7	80	6	10	11	12	13

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14 541.5 46.1 2466 17 US-10-795-148-2 15 541.5 46.1 2485 9 US-09-802-669-46 16 541.5 46.1 2485 15 US-10-619-220-46 17 541.5 46.1 2485 15 US-10-619-220-46 18 524 44.6 263 15 US-10-087-684-93 20 499 42.5 235 15 US-10-087-684-94 22 499 42.5 235 15 US-10-087-684-94 22 499 42.5 235 15 US-10-218-779-94 24 467 39.8 703 14 US-10-218-779-94 25 467 39.8 913 14 US-10-236-247-40 26 467 39.8 913 14 US-10-236-247-40 27 467 39.8 913 14 US-10-236-247-38 28 467 39.8 913 14 US-10-236-247-38 29 445.5 37.9 312 15 US-10-634-027-4 31 445.5 37.9 312 15 US-10-634-027-4 34 445.5 37.9 1997 16 US-10-634-027-2 35 444 37.8 1337 14 US-10-336-547-44 37 444 37.8 1337 14 US-10-366-547-44 38 444 37.8 1337 14 US-10-366-547-44 39 444 37.8 1337 14 US-10-366-547-44	444 37.8 1337 161 1 442.5 37.7 264 14 443.5 37.7 264 14 443.5 37.3 1948 10 443.5 37.3 1948 10 437.5 37.3 1948 10 437.5 37.3 1948 10 13.2 1216 14 437 37.2 1216 14 437 37.2 1216 14 437 37.2 1216 14 437 37.2 1216 14 11 20

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Length 379; Indels

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61 MVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 ONRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEBYFYIATQGPLPETIEDFWQ 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203 MVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQ 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRVVRKSHITGPLLVHCSAGVGRTG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ONRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 VFICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIQTK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 VFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 360
                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1174; DB 10; 100.0%; Pred. No. 3.4e-119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: RETHADES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 8 CORAGE
COMPUTER: IEM COMPATIBLE
OPERATING SYSTEM: IEM P.C. DOS 5.0
SOFTWARE: FASTEME TO SOFTWARE: FASTEME TO SOFTWARE TO SOFTWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/:
TELECHONE: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                         LENGTH: 379 amino acids
TYPE: amino acid
STRANDEDNESS: single
TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 218; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-09-095-478-8
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STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-09-095-478-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRVVRKSHITGPLLVHCSAGVGRTG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEBYFYIATQGPLPETIEDFWQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 354;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 1174; DB 10;
Best Local Similarity 100.0%; Pred. No. 3.1e-119;
Matches 218; Conservative 0; Mismatches 0; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09095478
| Publication No. US20030095970A1 |
| GENERAL INFORMATION: APPLICANT: PLOWMEN, Gregory TITLE OF INVENTION: PHOSPHATAGE SUPPPOS AND TITLE OF INVENTION: RELATED PRODUCTS AND SEQUENCES: 25 CORRESPONDENCE ADDRESS: ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPATER: FastSEQ for Windows 2.0
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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                       TELEPHONE: (213) 489-1600
TELEFAX: (713) 955-0440
TELEA: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-095-478-8
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308 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTG 367
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                                                                                                                                                                                                                                                                                                       248 MVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTOYFTVRVFO 307
                                                                                                                                                                                                                                                                                                                                                        121 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTG 180
                                                                                                                                                                             1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEBEYFYIATQGPLPETIEDFWQ
                                                                                                                                 0;
                                                                                          DB 10; Length 426;
                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368 VFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 405
                                                                                     100.0%; Score 1174; DB 10; ilarity 100.0%; Pred. No. 4e-119; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gregory
NOVEL PROTEIN TYROSINE
PHOSPHATASE SUPTP05 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPPOS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-095-478-2; Sequence 2, Application US/09095478; Publication No. US20030095970A1; GENERAL INFORMATION: APPLICANT: Plowman, Gregory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 463 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 67-3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                    ; MOLECULE TYPE: Peptide US-09-095-478-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
  linear
                                                                                     Query Match
Best Local Similarity
Matches 218; Conserv
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  TOPOLOGY:
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                                                                                                                                                                                             Gaps
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                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 3.8e-119;
Matches 218; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 VFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 VFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: PHOSPHATASE SUPTROSINE
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
TITLE OF SEQUENCES: 25
CORRESPONDENCES: 25
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION NUMBER: US/09/095,478
APPLICATION NUMBER: US/09/095,478
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NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELERA: (713) 955-0440
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l: 426 amino acids
amino acid
412 amino acids
                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                            TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-09-095-478-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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US-09-095-478-1
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                                                                                                                                          61 MVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQ 120
                                                                                                                                                                                                                                                           285 MVLENNCNVIAMITREIECCVIKCYSYWPISLKEPLEFEHFSVFLETFHVIQYFTVRVFQ 344
                                                                                                                                                                                                                                                                                                             121 IVKKSTGKSQCVKHLOFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTG 180
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                                                                                                           1 QNRDKNRYRDILLPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ
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             DB 10; Length 463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: INCYTE GENOMICS, INC.; AU-YOUNG, Janice K.
APPLICANT: BAUGHN, Mariah R.; DING, Li
APPLICANT: BAUGHN, Mariah R.; DING, Li
APPLICANT: BALLOTT, Vicki S.; GANDHI, Ameena R.
APPLICANT: GRIFFIN, Jennifer A.; HAFALLA, April J.A.
APPLICANT: KEARNEY, Liam, LEE, Ernestine A.
APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
APPLICANT: THORNIYN, Michael B.; TRIBOULEY, Catherine M.
APPLICANT: CHAWLA, Narinder K.; YANG, Junming
APPLICANT: THORNIYN, Michael B.; TRIBOULEY, Catherine M.
APPLICANT: THORNIYN, Michael G.;
YILLE OF INVENTION: PROTEIN PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040023245A1 7476861CD1
US-10-311-764-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Indels
                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             405 VFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 442
                                                                                                                                                                                                                                                                                                                                                                                                                   181 VFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 218
Score 1174; DB 10;
Pred. No. 4.4e-119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h
Similarity 78.8%; Pred. No. 3.6e-93;
71; Conservative 22; Mismatches 24;
                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REPERENCE: PI-0126 USN
CURRENT APPLICATION NUMBER: US/10/311,764
CURRENT APPLICATION NUMBER: US/10/311,764
CURRENT PILING DATE: 2002-12-16
PRIOR PTLING DATE: 2001-06-14
PRIOR PTLING DATE: 2000-06-16
PRIOR PTLING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: US 60/212,447
PRIOR APPLICATION NUMBER: US 60/215,210
PRIOR APPLICATION NUMBER: US 60/215,210
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-16
PRIOR FILING DATE: 2000-07-06
PRIOR FILING DATE: 2000-07-06
PRIOR PILING DATE: 2000-07-06
PRIOR PILING DATE: 2000-07-06
PRIOR PILING DATE: 2000-07-06
PRIOR FILING DATE: 2000-07-06
PRIOR FILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-21
NUMBER: OF SEQ ID NOS: 18
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/10311764 Publication No. US20040023245A1 GENERAL INFORMATION:
               100.0%;
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Best Local Similarity 78.84
Matches 171; Conservative
                                                                 Conservative
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ORGANISM: Homo sapiens
                  Query Match
Best Local Similarity
                                                                 218;
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                                                                    Matches
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                                                                                     243 VLENNSNVIAMITREIEGGIIKCYHYWDISLKKPLELKHFRVFLENYQILQYFIIRMFQV 302
                                                                                                                                              122 VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRIGV 181
                                                                                                                                                                      62 VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI 121
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Gaps
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                                                                                                                                                                                                                                 182 FICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIQTK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

56.9%; Score 668; DB 10;

Best Local Similarity 100.0%; Pred. No. 1.3e-64;

Matches 122; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Plowman, Gregory
JENTION: NOVEL PROTEIN TYROSINE
WONTION: PHOSPHATASE SUPTPO5 AND
VENTION: RELATED PRODUCTS AND
VENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FRATERO for Windows 2.0 CURRENT APPLICATION DATE: US/09/095,478 APPLICATION NUMBER: US/09/095,478
                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09095478
Publication No. US/20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WATBURG, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 amino acids
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Sulte .
CITY: Los Angeles
TWATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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CITY: LOS
STATE: CS
COUNTRY:
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                                     RESULT 9
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117 RVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGV 176
                                 61 RVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DFWGMMWENNCNVIAMITREIEGGVIKCCSYWPVSLKEPLEFKHFHVLLENFQITQYFVI
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                                                                                                                                                                                                     Sequence 5, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPTPOS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASISED for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acids
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STATE: California
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Best Local Similarity
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|21 GR 122
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US-09-095-478-5
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61 MVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFTVRVF 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 QIVKKSTGKSQCVKHLQFTKWPDHGTPASAD---FFIKYVRYVRKSHITGPLLVHCSAGV 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      321 GRSGTLICIDVVLGLISQDLEFDISDLVRCMRLQRHGMVQTE 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 GRIGVFICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIQTK 218
                                              TITLE OF INVENTION: NOVEL PROTEIN TYROSINE TITLE OF INVENTION: PHOSEPHARAE SUPPOS AND TITLE OF INVENTION: RELATED PRODUCTS AND TITLE OF INVENTION: METHODS NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS: ADDRESSE: Lyon & Lyon STREET: 633 West Fifth Street STREET: 633 West Fifth Street STREET: SULLE 4700
                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 90071-2066
COMPUTER READBABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/095,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
Sequence 7, Application US/09095478 Publication No. US20030095970A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 381 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 49.55
Matches 110; Conservative
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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California
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                                              GENERAL INFORMATION:
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MOLECULE TYPE:
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RESULT 10

GR 122

121

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61 MYLENNCHVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFTVRVF 119
                                                                                                                                                                                                                                                                                       APPLICANT: JUN-11chi Nezu
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
FILE REPERENCE: 06501-09900.
CURRENT APPLICATION NUMBER: US,10/060,065
CURRENT FILING DATE: 2002-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 QIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRT 179
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46.1%; Score 541.5; DB 14;
Best Local Similarity 47.0%; Pred. No. 1.7e-49;
Matches 103; Conservative 37; Mismatches 78; ]
                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2002-01-29

PRIOR APPLICATION NUMBER: PCT/JP00/05061

PRIOR APPLICATION NUMBER: US 60/159,590

PRIOR FILING DATE: 1999-10-18

PRIOR FILING DATE: 1999-10-18

PRIOR FILING DATE: 2000-02-17

PRIOR FILING DATE: 1999-07-29

PRIOR PILING DATE: 1999-07-29

PRIOR PILING DATE: 1999-07-29

PRIOR FILING DATE: 2000-01-11

PRIOR FILING DATE: 2000-05-02

PRIOR FILING DATE: 2000-05-02

PRIOR PILING DATE: 2000-05-02

PRIOR PILING DATE: 2000-05-02

PRIOR PILING DATE: 2000-05-03

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PATCHIN VET: 2.0
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Publication No. US20030082776A1
GENERAL INFORMATION:
APPLICANT: Ota, Toshio
APPLICANT: Isogai, Takao
APPLICANT: Nishikawa, Tetsuo
APPLICANT: Hayashi, Koji
APPLICANT: Hayashi, Koji
APPLICANT: Yamamoto, Jun-ichi
                                                                                                                                             Shizuko Ishii
Tomoyasu Sugiyama
Ai Wakamarsu
Keiichi Nagai
Tetsuji Otsuki
Shin-Ichi Funahashi
                                                                                                          Kaoru Otsuka
Jun-Ichi Yamamoto
                  Toshio Ota
Takao Isogai
Tetsuo Nishikawa
                                                                                      Koji Hayashi
                                                                                                                                                                                                                                                                                     Chiaki Senoo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CRGANISM: Homo sapiens
US-10-060-065-35
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-059-585-56
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ENRRKONRYKONILPYDATRVPLGDEGGYINASFIKIPVGKEEFVYIACQGPLPTTVGDFWQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 MIWEQKSTVIAMMTQEVEGEKİKCQRYWPNILGKTTMVSNRLRLALVRMQQLKGFVVRAM 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
46.1%; Score 541.5; DB 10; Length 3
Best Local Similarity 47.0%; Pred. No. 3.2e-50;
Matches 103; Conservative 37; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 GTLICIDVVLGLISQDLDFDISDLVRCMRLQRHGMVQTE 339
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                                                                                          Gregory
NOVEL PROTEIN TYROSINE
PHOSPHATASE SUPTPOS AND
RELATED PRODUCTS AND
                                                                                                                                                                                                                                                                                   STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTESO for Windows 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/115
RELEPHONE: (213) 489-1600
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/095,478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-060-065-35; Sequence 35, Application US/10060065; Publication No. US20030017480A1
                    Sequence 9, Application US/09095478 Publication No. US20030095970A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700
                                                                                                                                                                                 METHODS
                                                                               TITLE OF INVENTION: NOTITLE OF INVENTION: NOTITLE OF INVENTION: PHC TITLE OF INVENTION: REL TITLE OF INVENTION: MET NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS: SUPPERMENTED OF THE STATE OF THE STATE OF THE STATE OF T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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2277 MIWEQKSTVIAMMTQEVEGEKIKCQRYWPNILGKTTMVSNRLRLALVRMQQLKGFVVRAM 2336
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                                                                                                                                                                                                                                                         1; Gaps
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                                                                                                                                                                                                 Query Match
46.1%; Score 541.5; DB 14; Length 2466;
Best Local Similarity 47.0%; Pred. No. 4e-49;
Matches 103; Conservative 37; Mismatches 78; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: POETRIC, JASNA
APPLICANT: PERECIC, JASNA
APPLICANT: JERECIC, JASNA
APPLICANT: LORENTE, GUSTAVO A.
APPLICANT: UFFER, ROWAN
TITLE OF INVENTION: USE OF BIOMOLECULAR TARGETS IN THE
TITLE OF INVENTION: TREATMENT AND VISUALIZATION OF TUMORS
THEN REPERENCE: ACT 02
CURRENT APPLICATION NUMBER: US/10/795,148
CURRENT FILING DATE: 2004-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2397 GTLICIDVVLGLISQDLDFDISDLVRCMRLQRHGMVQTE 2435
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NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/452,169
PRIOR FILING DATE: 2003-03-04
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10795148; Publication No. US20040224337A1; GENERAL INFORMATION:
                                                                       LENGTH: 2466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-980-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: H. sapiens
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Best Local Similarity
Matches 103; Conserv
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APPLICANT: Franch, Petra
APPLICANT: Franch, Petra
APPLICANT: Franch, Pontus
APPLICANT: Hellman, U1
APPLICANT: Hellman, U1
APPLICANT: Hellman, Carl-Henrik
TITLE OF INVENTION: PARC, A GIPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
FILE REPERBNES: L0461/7030
CURRENT APPLICATION NUMBER: U5/10/17,980
CURRENT FILING DATE: 2002-06-21
PRIOR PRICATION NUMBER: U5/09/080,855
PRIOR PAPLICATION NUMBER: 08/09/080,855
PRIOR APPLICATION NUMBER: 08/09/080,859
PRIOR FILING DATE: 1999-05-18
PRIOR FILING DATE: 1999-05-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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47.0%; Pred. No. 1.7e-49;
"...marches 78; Indels
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                     APPLICANT: Sugiyama, Tomoyasu
APPLICANT: Wakamatsu, Ai
APPLICANT: Nagai, Keiichi
APPLICANT: Orsuki, Tetsuji
APPLICANT: Funahashi, Shin-Ichi
APPLICANT: Senco, Chiaki
APPLICANT: Nezu, Jun-Ichi
APPLICANT: Nezu, Jun-Ichi
TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
                                                                                                                                                                                                                                      THILE OF INVENTION:

CURRENT APPLICATION NUMBER: US/10/059,585

CURRENT APPLICATION NUMBER: US/10/059,585

CURRENT APPLICATION NUMBER: US/10/050,586

PRIOR APPLICATION NUMBER: DCT/JP00/05060

PRIOR FILING DATE: 2000-07-28

PRIOR FILING DATE: 2000-07-28

PRIOR FILING DATE: 2000-02-17

PRIOR FILING DATE: 1999-10-18

PRIOR PRIOR DATE: 2000-011

PRIOR PRIOR DATE: 2000-011

PRIOR PILING DATE: 2000-01-11

PRIOR PILING DATE: 1099-10-13

PRIOR PILING DATE: 1099-10-13

PRIOR PILING DATE: 1099-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 12, Application US/10177980
; Publication No. US20030166232A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 103; Conservative
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Best Local Similarity
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US-10-177-980-12
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APPLICANT: Dari, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Wayatt, Jacqueline
APPLICANT: Wayatt, Jacqueline
APPLICANT: Wayatt, Jacqueline
APPLICANT: Watthern and Antisense Compound Modulation of Fas Mediated Signaling
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
TITLE REFERENCE: ISPH-545
CURRENT APPLICATION NUMBER: US/09/802,669
FRIOR FILING DATE: 2001-03-09
PRIOR PLING DATE: 2000-09-18
PRIOR PLING DATE: 1999-04-12
PRIOR PLING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 46
LENGTH: 2485
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46.1%; Score 541.5; DB 9; Length 2485;

Best Local Similarity 47.0%; Pred. No. 4.1e-49;

Matches 103; Conservative 37; Mismatches 78; Indels 1;
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RESULT 15
US-09-802-669-46
Sequence 46, Application US/09802669
Patent No. US2002004490A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
CRGANISM: Homo sapiens
US-09-802-669-46
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Search completed: December 1, 2004, 12:52:39
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Sequence 3, Appli Sequence 12, Appli Sequence 12, Appli Sequence 2, Appli Sequence 46, Appli Sequence 16, Appli Sequence 17, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 2, Appli Sequence 38, Appli Sequence 1, Appli
                                                                        1, 2004, 12:07:42 ; Search time 23.5848 Seconds
(without alignments)
612.993 Million cell updates/sec
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/cgm2_6/prodata/1/iaa/5B_COMB.pep:*
/cgm2_6/prodata/1/iaa/6A_COMB.pep:*
/cgm2_6/prodata/1/iaa/6B_COMB.pep:*
/cgm2_6/prodata/1/iaa/PcTUS_COMB.pep:*
/cgm2_6/prodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-446-345-38
US-08-446-345-38
US-08-991-258A-3
US-08-991-258A-3
US-08-991-258A-3
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US-08-991-953A-3
US-08-991-953A-3
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US-08-991-953A-3
US-08-991-953A-3
US-08-991-953A-3
US-08-991-953A-5
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                          December
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467
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No.
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Sequence 5, Appli Sequence 14, Appli Sequence 14, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli Sequence 1, Appli Sequence 11, Appli Sequence 11, Appli Sequence 18, Appli Sequence 8, Appli Sequence 8, Appli Sequence 9, Appli Sequence 4, Appli Sequence 4, Appli	S FOR NOVEL PROTEIN	.h 2465;
246 4 US-09-848-294-9 254 2 US-09-848-294-9 1254 2 US-09-848-2914 1259 1 US-08-65-92-14 1350 2 US-08-201-697-4 1439 2 US-08-201-697-4 1439 2 US-08-447-464-3 1501 2 US-08-447-464-3 1501 2 US-08-687-244A-2 1501 2 US-08-16-679-3 11501 2 US-08-16-679-8 1174 2 US-08-91-24A-8 1174 2 US-08-91-24A-8 1452 2 US-08-91-258A-4 1452 2 US-08-71-4	ALIGNMENTS pplication US/08596291 11075 WAGNEZ, LEONEL JORGE SARAS, JAN CLAESSON-WELSH, LENA HELDIN, CARL-HENRIK WENTION: WENT	46.1%; Score 541.5; DB 2; Length 47.0%; Pred. No. 3.4e-53;
28 4 32.5 30 4 43.5 31 43.1.5 32 43.1.5 33 4 423 33 4 423 34 427.5 36 4 427 39 427 30 44 427.5 36 4 427 30 4 427.5 36 6 427.5 36 7 427.5 36 8 427.5 36 9 427.5 36 9 428.3 429.7 420.0 420.	RESULT 1 US-08-596-291-3 Sequence 3, Application US/08596291 Patent No. 5821075 GENERAL INFORMATION: APPLICANT: GONEZ, JAN APPLICANT: CLAESSON-WELSH, LENA TITLE OF INVENTION: PRIMARY STR TITLE OF INVENTION: PRIMARY STR TITLE OF INVENTION: PRIMARY STR TITLE OF INVENTION: PRIMARY STR TITLE OF INVENTION: TYPOSINE PH NUMBER OF SEQUENCES: 4 CORRESPONDENCES ADDRESS: ADDRESSES: WOLF, GREENTELD & STREET: MASSACHUSETTS COUNTRY: BOSTON STREET: BOSTON STREET: GOO ATLANTIC AVENUE CONFUTER: IBM PC COMPATIBLE CONPUTER: IBM PC COMPATIBLE COMPUTER: BOSTON SOFTWARE: PATENTIN PARA APPLICATION NUMBER: US/08/596 FILING DATE: 09-AUG-1996 CLASSIFICATION DATA: APPLICATION NUMBER: US/08/596 FILING DATE: 01-SEP-1993 ATTORNEY/AGENT INFORMATION: NAME: GATES, EDWARD R. REGISTRATION NUMBER: US/08/596 FILING DATE: 01-SEP-1993 ATTORNEY/AGENT INFORMATION: NAME: GATES, EDWARD R. REGISTRATION NUMBER: US/08/596 FILING DATE: 01-SEP-1993 ATTORNEY/AGENT INFORMATION: NAME: GATES, EDWARD R. REGISTRATION NUMBER: US/08/596 TELEFAX: 92-1742 ESEKTEL INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 2465 amino acids TYPE: amino acid TYPE: protein US-08-596-291-3	Query Match Best Local Similarity

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47.0%;
Best Local Similarity 47.0%
Matches 103; Conservative
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, ORGANISM: Homo sapiens
US-09-080-855-12
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US-09-566-076-12
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US-09-080-855-12
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                                                       APPLICANT: GONEZ, LEONEL JORGE
APPLICANT: SARAS, JAN
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                 61 MVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFTVRVF 119
                                                                                                                                                                120 QIVKKSIGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRT 179
                                   1 ONRDKARYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATOGPLPETIEDFWQ
      1; Gaps
      Indels
                                                                                                                                                                                                                                                        GVFICVDVVFSAIEKNYSFDIMNIVTOMRKORCGMIQTK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,804
      78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C. STREET: 600 ATLANTIC AVENUE
          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/596,291
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
FILING DATE: 01-SEP-1993
FILING APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: GATES, EDWARD R. REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: LO461/7003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09100804
Patent No. 6066472
          37;
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           103; Conservative
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MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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STATE: MA
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46.1%; Score 541.5; DB 3; Length 2465;

Query Match

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GRUERAL INFORMATION:

GROEFAL INFORMATION:

APPLICANT: Saras, Jan
APPLICANT: Franzn, Petra
APPLICANT: Hellman, Ulf
APPLICANT: Genez, Leonel Jorge
APPLICANT: Hellman, Ulf
APPLICANT: Hellman, Ulf
APPLICANT: Hellman, Ulf
APPLICANT: Hellman, Ulf
APPLICANT: Hellman, Ulf
APPLICANT: Hellman, Ulf
APPLICANT: WINDER: Usenel Jorge
APPLICANT: WINDER: Usenel Jorge
APPLICANT: WINDER: Usenel Jorge
CURRENT APPLICATION NUMBER: Usenel Jorge
CURRENT APPLICATION NUMBER: 08/805,583
EARLIER APPLICATION NUMBER: 08/805,583
MUMBER: OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12.
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                                                                                                    61 MVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFTVRVF 119
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                                                                         QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ
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47.0%; Pred. No. 3.4e-53;
iive 37; Mismatches 78;
Pred. No. 3.4e-53;
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                                         37;
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les 103; Conservative
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APPLICANT: Franzn, Petra
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2276
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Patent No. 6204055
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TILE REFERENCE: ISPH-0351
CURRENT APPLICATION: Autisense Compound Modulation of Fas Mediated Signaling
CURRENT APPLICATION NUMBER: US/09/290,640
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 46
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; Pred. No. 3.4e-53;
37; Mismatches 78;
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             PELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                               46.1%;
47.0%;
                                                                       TELEX: 92-1742 EZEKIEL
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2466 amino acids
                                : 617/720-3500
617/720-2441
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 47.0%
Matches 103; Conservative
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Matches 103; Conservative
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MOLECULE TYPE: protein
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                                                                                                                                                                    TYPE: amino acid
                                TELEPHONE: TELEFAX: 6
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TYPE: PRT
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APPLICANT: Aspenstrm, Pontus
APPLICANT: Hellman, Ulf
APPLICANT: Hellman, Ulf
APPLICANT: Gonez, Leonel Jorge
APPLICANT: Heldin, Carl-Henrik
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
CURRENT APPLICATION NUMBER: US/09/566,076
EARLIER APPLICATION NUMBER: 09/080,855
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2277 MIWEQKSTVIAMMIQEVEGEKIKCQRYWPNILGKTIMVSNRLRLALVRMQQLKGFVVRAM 2336
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EXPRESSION OF NUCLECTIDE SEQUENCES FOR NOVEL PROTEIN
TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 MVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFTVRVF 119
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COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
ATTORNEY AGENT INFORMATION:
NAME: TWOMEY, MICHAEL J.
REGISTRATION NUMBER: P-38,349
REFERENCE/DOCKET NUMBER: L0461/7000WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 01-SEP-1994
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GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CORGANISM: Homo sapiens
US-09-566-076-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BOSTON
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PCT-US94-09943-2
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APPLICANT:
APPLICANT:
APPLICANT:
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Query Match
Best Local Similarity 42.3'
Matches 96; Conservative
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APPLICANT: TONKS, Nicholas K.

APPLICANT: TONKS, Nicholas K.

APPLICANT: TONKS, Nicholas K.

TITLE OF INVENTION: Protein Tyrosine Phosphotase Which Localizes to Focal

TITLE OF INVENTION: Adhesions and Uses Therefor

CURRENT APPLICATION NUMBER: US/09/848,294

CURRENT FILING DATE: 1990-01-22

PRIOR PELING DATE: 1990-01-22

PRIOR PELING DATE: 1990-01-42

PRIOR FILING DATE: 1990-03-04

PRIOR FILING DATE: 1991-03-04

PRIOR FILING DATE: 1991-03-04

PRIOR PRIOR APPLICATION NUMBER: 07/663,579

PRIOR PRIOR APPLICATION NUMBER: 07/494,036

PRIOR APPLICATION NUMBER: 07/494,036

PRIOR FILING DATE: 1990-03-14

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2236 ENRRKNRYKNILPYDATRVPLGDEGGYINASFIKIPVGKEEFVYIACQGPLPTTVGDFWQ 2295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                              APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Wyatt, Jacqueline
TITLE OF INVENTION. Antisense Modulation of Fas Mediated Signaling
FILE REPRENCE: ISPH-0502
CURRENT APPLICATION NUMBER: US/09/665,615B
CURRENT FILING DATE: 2000-09-18
PRIOR PEPLICATION NUMBER: US 09/290,640
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 2485;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 46.1%; Score 541.5; DB 4; Best Local Similarity 47.0%; Pred. No. 3.4e-53; Matches 103; Conservative 37; Mismatches 78;
                                            Sequence 46, Application US/09665615B Patent No. 6653133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-848-294-2
; Sequence 2, Application US/09848294
; Patent No. 6479640
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                    ), ORGANISM: Homo sapiens
US-09-665-615B-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homosapiens US-09-848-294-2
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TYPE: PRT
                                     US-09-665-615B-46
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                                                                                                                                                                                                                                                                                                                54 TIEDFWQMYLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEH--FSVFLETFHVT 111
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                                                                                              1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYI------RIVNHEBEYFYIATQGPLPE
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39.4%; Score 462.5; DB 1; Length 278;
Best Local Similarity 43.0%; Pred. No. 2.3e-45;
Matches 98; Conservative 38; Mismatches 79; Indels 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Wiggins, Roger C.
APPLICANT: Thomas, Peedikayil E.
TITLE OF INVENTION: Mammalian Glomerular Epithelial Protein
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                   171 HCSAGVGRIGVFICVDVVFSAIBKNYSFDIMNIVTQMRKQRCGMIQT 217
                                                                                                                                                                                                                                                                                                                                                                                                               39.8%; Score 467; DB 4; Length 913; 42.3%; Pred. No. 3.7e-45; Live 35; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 25-FEB-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-UM 9783
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Patent No. 5705623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cartryb A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UM
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 535-8001
TELEFAX: (619) 535-8001
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 278 amino acids amino acids
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MEDIUM TYPE: Floppy
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California
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GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas K.

APPLICANT: Tonks, Nicholas K.

TITLE OF INVENTION: Protein Tyrosine Phosphotase Which Localizes to Focal
TITLE OF INVENTION: Adhesions and Uses Therefor
TITLE OF INVENTION: Adhesions and Uses Therefor
FILE REFERENCE: CSHL90-04FZA

CURRENT APPLICATION NUMBER: 108/09/848,294

CURRENT FILING DATE: 2001-05-03

PRIOR APPLICATION NUMBER: 09/235,251

PRIOR FILING DATE: 1996-10-22

PRIOR FILING DATE: 1996-12-04

PRIOR FILING DATE: 1996-12-04

PRIOR FILING DATE: 1996-12-04

PRIOR PELLING DATE: 1991-03-01-16

PRIOR FILING DATE: 1991-03-01-16

PRIOR FILING DATE: 1991-03-01-16

PRIOR FILING DATE: 1990-03-01-14

NUMBER OF SEQ ID NOS: 13

SCOTTWARE FERENCE: FERENCE OF Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 IEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEH--FSVFLETFHVTQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 YFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHI-TGPLLVH 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
39.4%; Score 462; DB 4; Length 244; 42.0%; Pred. No. 2.2e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 CSAGVGRIGVFICVDVVPSALEKNYSFDIMNIVTOMRKORCGMIQT
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Patent No. 5912138
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35; Mismatches
                                                                                               RESULT 11
US-05-448-294-7
'Sequence 7, Application US/09848294
'Patent No. 6479640
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Best Local Similarity 42.0
Matches 95, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homosapiens
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                         173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 YFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHI-TGPLLVH 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 AYVSREMLVTNTQTGEEHTVTHLQYVAWPDHGIPDDSSDFLEFVNYVRSLRVDSEPVLVH 172
     VRVFQIV-KKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVR----YVRKSHITGPLLV 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----RIVNHEEEYFYIATQGPLPET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                               222 HCSAGVGRTGTFIALDRILQQLDSKDSVDIFGIVYAMRKERVWMVQTE 269
                                                                                               171 HCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 39.4%; Score 462; DB 2; Length 231; Best Local Similarity 42.0%; Pred. No. 2.1e-45; Matches 95; Conservative 35; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 CSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,345
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/234,440
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                            NOVEL PROTEIN PHOSPHOTYROSINE
PHOSPHATASES PTP-D1
41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: Pennie & Edmonds
: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                          Sequence 37, Application US/08446345;
Patent No. 5831009
GENERAL INFORMATION:
APPLICANT: Ullrich, Axel
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Niels P.H.
TITLE OF INVENTION: PHOSPHATASES PT
NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid STRANDEDNESS: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RY: U.S.A.
10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                           US-08-446-345-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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54 TIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHV--- 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 SEDCTIAYVSMLVTNTQTGEEHTVTHLQYVAWPDHGIPDDSSDFLEFVNYVRSLRVDSEP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 TCAQFWQVVWDQXLSLIVMLTTLTERGRTKCHQYWP---DPPDVMNHGG-----FHIQCQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ONRDKONRYRDILPYDSTRVPLGKOKDYINASYI-----RIVNHEEEYFYIATQGPLPE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Sequence 2, Application US/08854585

Sequence 2, Application US/08854585

Patent No. 6114140

PAPLICANT: Tonks, Nicholas K. and stman, Arne

TITLE OF INVENTION:

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLVHCSAGVGRIGVFICVDVVFSAIBKNYSFDIMNIVTQMRKQRCGMIQT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Marshall, O'Toole, Gerstein, Murray & Borun 233 South Wacker Drive, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

38.8%; Score 456; DB 2;
Best Local Similarity 41.7%; Pred. No. 1.1e-44;
Matches 96; Conservative 35; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Borun, Michael F.
REGISTRATION NUMBER: 25,447
REFERENCE/DOCKET NUMBER: 27866/31954
                                                                                                                                         NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-03Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/237,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 60606
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/854,585 FILING DATE:
                                       DATA:
TER: 08/685,992
                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,
FILING DATE: JULY 25, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-144-925-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 TCAQFWQVVWDQKLSLIVMLTTLTERGRIKCHQYWP---DPPDVMNHGG-----FHIQCQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 TQYFTVRVFQ--IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHI-TGP 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 QNLDKNRYKDVLPYDTTRVLLQGNEDYINASYVNMEIPAANLVNK-----YIATQGPLPH 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYI-----RIVNHEEEYFYIATQGPLPE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 LLVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTOMRKQRCGMIQT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 38.8%; Score 456; DB 2; Length 242; Best Local Similarity 41.7%; Pred. No. 1.1e-44; Matches 96; Conservative 35; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21, Application US/09144925
; Patent No. 5951979
; GENERAL INFORMATION;
GENERAL INFORMATION;
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Lexington
CITY: Lexington
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FREEKEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,992
FILING DATE: 25-UU-1996
CLASSIFICATION: 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIF: 02421-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastESQ for Windows Version 2.0b
CURBENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,925
                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-03
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 242 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-08-685-992-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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DEWOMYLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTV 116
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                                                                                                                                                                                                                                                                                           1 ONRDKNRYRDILPYDSTRVPLG----KNKDYINASYIRIVNHEEEYFYIATQGPLPETIE 56
                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                37.8%; Score 444; DB 3; Length 1337; Similarity 41.2%; Pred. No. 3e-42; Onservative 42; Mismatches 79; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 SAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRNT APPLICATION DATA:
APPLICATION NAMBER: US/09/447,533
FILING DATE: 23-No. 6552169-1999
CLASSIFICATION: CURRNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DENSITY ENHANCED PROTEIN TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                       79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Rosenman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 200125.402C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group PLLC STREET: Suite 6300, 701 Fifth Avenue CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tonks, Nicholas K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 2, Application US/09447533
; Patent No. 6552169
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
              TELEPHONE: 312-474-6300

TELEFAX: 312-474-6300

INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 1337 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-684-585-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Washington COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                     93;
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US-09-447-533-2
                                                                                                                                                                                                                Query Match
Best Local S:
Matches 93
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                                                                                                                                                                 117 RVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKY---VR-YVRKSHITGPLLVHC 172
                                                       1 QNRDKNRYRDILPYDSTRVPLG----KNKDYINASYIRIVNHEEEYFYIATQGPLPETIE 56
                             Gaps
                           12;
                                                                                                                                                                                                                                        Length 1337;
                                                                                                                                                                                                                        173 SAGVGRIGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 218
                           Indels
37.8%; Score 444; DB 4; L
41.2%; Pred. No. 3e-42;
tive 42; Mismatches 79;
Query Match 37.8%
Best Local Similarity 41.2%
Matches 93; Conservative
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1, 2004, 12:07:39; Search time 76.4912 Seconds (without alignments) 1022.379 Million cell updates/sec

1174 1 QNRDKNRYRDILPYDSTRVP.....DIMNIVTQMRKQRCGMIQTK 218 Title: Perfect score: Sequence:

US-09-095-478A-7_COPY_188_405

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB s Maximum DB s

seq length: 0 seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2001as:* geneseqp2001as:* A_Geneseq_23Sep04:* 1: qenesemnloon-Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s;*

STIMMARTES

	Ď,	Aaw89251 Mouse PTP	σ		Human	6 Human	4 Human	Human		Novel	6 Novel	Novel		Rat PT	Abu70688 Human adi	Amino	8 Amino	Aar71498 Human pro	Aaw75999 Intracell	_	Aab19343 Amino aci	Human	Human	Human	3 Polymer	2 Mouse PT
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ALIGNMENTS

PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease. AAW89251 standard; protein; 405 AA. 98WO-US008439 (first entry) Mouse PTP05 isoform #2. W09849317-A2. 27-APR-1998; 10-MAR-1999 05-NOV-1998 AAW89251; Mus sp. RESULT 1

97US-0044428P. 97US-0047222P. 97US-0049477P. 97US-0049914P. 97US-0063595P. 28-APR-1997; 20-MAY-1997; ; 1991-NUL-11 ; 1991-NUL-11

18-JUN-1997; 23-OCT-1997;

(SUGE-) SUGEN INC.

Markby D; Onrust S, Peles E, Plowman GD, Clary D, Jallal B, Courtneidge SA, App H, Hui TH; Clary D,

WPI; 1999-009434/01. N-PSDB; AAV81746.

New nucleic acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.

Claim 2; Page 158-160; 193pp; English.

The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The present sequence represents mouse PTP05. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify

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substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therety (optionally after mutation). Ab are used to determine the
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100.0%; Pred. No. 9.9e-127;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 218; Conservative
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20-MAY-1997;
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continue present invention describes isolated, enriched or published muciello acids encoding PTPOS, PTPOS, PTPOS, PTPOS, PTPOS acids encoding PTPOS, TPTPOS, PTPOS. The above proteins. The present sequence represents mouse PTPOS. The above proteins, other than a protein tyrosine phosphatases (PTPS) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, concluding NBP) in vivo or in vitro. These substances are used to identify prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukamia and tymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, corrine/threonine kinase) are used to promote neuronal survival, corrine/threonine kinase) are used to promote neuronal survival, correcting can be used as probes to identify and clone related sequences; conceins can be used as probes to identify and clone related sequences; therapy (optionally after mutation). Ab are used to determine the
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       protein tyrosine phosphatases for treatment and prevention
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           New nucleic acid encoding specific protein tyrosine
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Matches 218; Conservative 0; Mismatches
                                                                                                                   present invention describes isolated,
                                                                                   2; Page 155-157; 193pp; English
                                             cancer and neurodegenerative disease.
                                identifying specific modulators
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11-JUN-1997;
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Jallal B, , Hui TH;

Plowman GD, Clary D, J Courtneidge SA, App H,

SUGEN INC.

(SUGE-)

WPI; 1999-009434/01

N-PSDB; AAV81744

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that involve the proteins, particularly cancer (e.g. leakaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzahemer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA, to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
                                                                                                                                                                                                                                                                                                                                                       The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The present sequence represents mouse PTP05. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways
                                                                                                                                                                                                                                                            identifying specific modulators for treatment and prevention of
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                                                                                                                                                                                                                                     New nucleic acid encoding specific protein
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                                                                                                                                                                                                                                                                               cancer and neurodegenerative disease.
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97US-0049756P.
97US-0049914P.
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11-JUN-1997;
18-JUN-1997;
23-OCT-1997;
                                                                                                                   Plowman GD,
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MVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQ 120 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTG 180 345 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTG 404 QNRDKNRYRDILLPYDSTRVPLGKNKDYINASYIRIVNHEBEYFYIATQGPLPETIEDFWQ 285 MVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEPEHFSVFLETFHVTQYFTVRVFQ 1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ ; 0 100.0%; Score 1174; DB 2; Length 463; 100.0%; Pred. No. 1.2e-126; Indels ; 0 0; Mismatches Conservative Local Similarity nes 218; Conserv Sequence 463 AA; 121 Query Match 61 Best Loca Matches d à d δ qq

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Gaps

344

VFICUDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 218 VFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 442

à q

Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis; atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer; psoriasis; thromobocytopaenia; developmental disorder; Reiter's syndrome; renal tubular acidosis; anaemia; mental retradation; Alzheimer's disease; neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis; Human kinase and phosphatase (KPP-39) protein. Ā AAE37994 standard; protein; 261 (first entry) 06-NOV-2003 AAE37994; AAE37994 RESULT

acquired immune deficiency syndrome; immunosuppressive; Crohn's disease; nootropic; transgenic; dermatitis; multiple sclerosis; diabetes mellitus; allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome; osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological; gene therapy; asthma; anticonvulsant; uropathic; pancreatitis Goodpasture's syndrome autoimmune disorder; inflammatory disorder; AIDS;

Homo sapiens.

Markby D;

WO2003050084-A2

19-JUN-2003

useful

06-DEC-2002; 2002WO-US039126

07-DEC-2001; 2001US-0340235D. 19-DEC-2001; 2001US-0343007P. 21-DEC-2001; 2001US-0343546P. 04-FEB-2002; 2002US-0354388P.

2002US-0357675P 15-FEB-2002;

(INCY-) INCYTE GENOMICS INC,

Marquis JP; Gorvad AE; Griffin JA, Marquis ', Lee S, Hawkins PR; AD, Swarnakar A, Go Ramkumar J, Jin P, ' r-Mason PM, Khare R, Sprague WW, Zebarjadian Y; Lehr-Mason Wilson AD, Emerling BM, Kable AL, Emeritus Hafalia AJA, Emeritus '- MR. Chawla NK, Spy Baughn MR, Char. Kable AE,

2003-532894/50. N-PSDB; AAD57366 New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AlDS, allergy or anemia), multiple sclerosis, osteoarthritis, cancer or hepatitis.

Claim 1; Page 242; 282pp; English.

diagnosting, treating or preventing disorders associated with aberrant expression of KPP, particularly cell proliferative disorders (e.g. expression of KPP, particularly cell proliferative disorders (e.g. expression of KPP, particularly cell proliferative disorders (e.g. exteriosolerosis, atherosolerosis, cirrhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary circonores, caidosis, anaemia or mental retardation), neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune, inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome, allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's clisease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome, cout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome, syndrome, rheumatoid arthritis, sjogran's syndrome, uveitis), or viral, bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP is useful in assessing the effects of exogenous compounds on the The invention relates to an isolated polypeptide, which is a human kinase expression of nucleic acids and kinases and phosphatases. KPP gene is useful in gene therapy and for creating transgenic animals to model human disease. The present sequence is human KPP protein and phosphatase (KPP). KPP agonists and antagonists are useful

Sequence 261 AA;

Gaps ., Length 261; 24; Indels . 9 79.7%; Score 936; DB 6; 78.8%; Pred. No. 2e-99; cive 22; Mismatches 2 Matches 171; Conservative Query Match Best Local Similarity

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NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQM

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182 204

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AAE37996;

AAE37996 RESULT

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gout, Graves disease, Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral, bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP is useful in assessing the effects of exogenous compounds on the expression of nucleic acids and kinases and phosphatases. KPP gene is useful in gene therapy and for creating transgenic animals to model human disease. The present sequence is human KPP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, protein phosphatase, PP-4; immune system disorder; AIDS; allergy; neurological disorder; developmental disorder; Alzheimer's disease; cell proliferative disorder; Huntington's disease; arteriosclerosis; renal tubular acidosis; gonadal dysgenesis; cancer; adenocarcinoma;
diabetes mellitus, glomerulonephritis, Goodpasture's syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 VLENNSNVIAMITREIEGGIIKCYHYWPISLKKPLBLKHFRVFLENYQILQYFIIRMFQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 NREKNRYRDILPYDSTRVPLGKSKDYINASYIRIVNCGEEYFYIATQGPLLSTIDDFWQM
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                                                                                                                                                                                                                                                                                                                                                                                                                                 79.7%; Score 916; DB 6; Length 412; 78.8%; Pred. No. 3.8e-99; ive 22; Mismatches 24; Indels
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/note= "Protein-tyrosine phosphatase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 218
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362. .379
/label= Transmembrane_domain
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22-JUN-2000; 2000US-0213746P.
29-JUN-2000; 2000US-021510P.
06-JUL-2000; 2000US-0218629P.
12-JUL-2000; 2000US-0218080P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 171; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            Sequence 412 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, kinase; phosphatase; KPP; cell proliferative disorder; hepatitis; atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer; psoriasis; thromobocytopaemia; developmental disorder; Reiter's syndrome; renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease; neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis; autoimmune disorder; Inflammatory disorder; AIDS; Goodpasture's syndrome; acquired immune deficiency syndrome; immunosuppressive; Crohn's disease; nootropic; transgenic; dermatitis; multiple sclerosis; diabetes mallitus; allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome; osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological; gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kable AE, Chien D, Wilson AD, Swarnakar A, Gorvad AE;
Hafalia AJA, Emerling BM, Ramkumar J, Jin P, Griffin JA, Marquis JP,
Baughn Mr, Chawla NX, Lehr-Mason PM, Khare R, Lee S, Hawkins PR;
Becha SD, Lee SY, Sprague WW, Zebarjadian Y;
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               122 VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV
                                                            FICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human kinase and phosphatase (KPP-41) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE37996 standard; protein; 412
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21-DEC-2001, 2001US-0343546P.
04-FEB-2002; 2002US-0354388P.
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AA.

ABG30845 standard; protein; 398

ABG30845

(first entry)

21-OCT-2002

ABG30845;

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The present sequence is minimary process. By the present sequence is minimary to the process. The present sequence is minimary to the process. The present sequence is minimary to the sequence of immune system disorders nearly proliferative disorders. Examples of immune system disorders and call proliferative disorders. Examples of immune system disorders include acquired immune deficiency syndrome (AIDS), severe combined immunodeficiency disease (SCID), adult crespiratory distress syndrome, allergies, amyloidosis, anamia, asthma, atherosclerosis, Crohn's disease, allergies, amyloidosis, anamia, asthma, catherosis, myasthenia gravis, myocardial or pericardial inflammation, osteoporosis, myocardial or pericardial inflammation, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome, coffeoarthritis, Sjogren's syndrome, soleroderma, systemic coffeoarthritis, Sjogren's syndrome, soleroderma, systemic coffeoarthritis, Siogren's syndrome, soleroderma, systemic retardation and other developmental disorders including mood, anxiety, and schizophrenic disorders, seasonal affective disorders such as akathesia, amnesia, caratonia, dyskinesia, developmental disorders include e.g. renal tubular acidosis, Duchenne and Electrive disorders include e.g. renal tubular acidosis, Duchenne and Becker muscular dystrophy, gonadal dyspenseis, hypothyroidsiam; cell colliferative disorders include e.g. actinic keratosis, arteriosclerosis, arteriosclerosis, hursitis, cirrhosis, hepatitis, psoriasis and cancer including adenocarcinoma, leukaemia. The polypoptide and polyburoleocider or arallysing achome of a risking or a relither marking and polymoleocidide.
                                                                                                          , Ding L, Elliott VS, Gandhi AR, Griffin JA;
Lee EA, Lu Y, Nguyen DB, Patterson C;
Sanjamwala MS, Stewart EA, Tang YT, Thornton M;
K, Yang J, Yao MG, Yue H;
                                                                                                                                                                                                                                                                                                                                Novel polypeptide, useful for diagnosing, treating or preventing disorders of growth and development, immune system, neurological and cell proliferation diseases, comprises cancer protein phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   are further useful for analysing proteome of a tissue or a cell type, for screening an agonist/antagonist, a compound that specifically binds to it or its modulator. The polymuclectide is useful for creating knockin humanised animals (pigs) or transgenic animals (mice or rats) to model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human disease, for generating a transcript image of a tissue or cell
type, which represents the global pattern of gene expression by a
particular tissue or cell type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is human protein phosphatase (PP)-4. PP
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                                                                                                            Baughn MR, Ding L
Kearney L, Lee EA,
Reddy R, Sanjanwa
  21-JUL-2000; 2000US-0220117P.
                                                   (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                             Tribouley CM, Walia NK,
                                                                                                                                                                                                                                                   2002-090206/12.
                                                                                                                                                                                                                                                                          N-PSDB; AAD24022
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                                                                                                                                   Hafalia A,
Ramkumar J,
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VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI 121 VKKSTGKSQCVKHLOFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV 181 NREKNRYRDILPYDSTRVPLGKSKDYINASYIRIVNCGEEYFYIATQGPLLSTIDDFWQM 2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEBEYFYIATQGPLPETIEDFWQM . 0 Length 420; 24; Indels FICUDUVFSALEKNYSFDIMNIVTOMRKORCGMIOTK 218 79.7%; Score 936; DB 5; 78.8%; Pred. No. 3.9e-99; ive 22; Mismatches 24; Conservative Query Match Best Local Similarity Matches 171; Conserv Sequence 420 AA; 183 62 122 303 182 g 엄 g ò à ð

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polypeptide. The inventions to a mean tytosine phosphatase to a medicament for modulating the activity of human tyrosine phosphatase in a disease such as obesity, diabetes, a central nervous system (CNS) disorder, chronic obstructive pulmonary disease, cardiovascular disorder or cancer. The invention is useful for treating a human tyrosine phosphatase of dysfunction related disease, preferably the above mentioned diseases. The invention is useful for treating the above mentioned diseases. The invention is useful for treating the above mentioned discases. The invention is useful for treating the above mentioned discases. The croke, Alzheimer's disease, and Huntington's disease, and the cardiovascular disorder is selected from congestive heart failure and myocardial infarction. The molecules of the invention are useful in diagnostic assays for detecting diseases and abnormalities or autations in the polynucleotide coding the polypeptide of the invention. The present amino acid sequence represents the human tyrosine phosphatase protein #1 of the invention. This sequence is encoded by the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human tyrosine phosphatase polypeptide, the regulation of which is useful for treating obesity, diabetes, cardiovascular or central nervous system disorder, chronic obstructive pulmonary disease and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                       central nervous system disorder; CNS; cardiovascular disorder; stroke; chronic obstructive pulmonary disease; cancer; multiple sclerosis; Alzheimer's disease; Huntington's disease; congestive heart failure; myocardial infarction; chromosome 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                       tyrosine phosphatase; obesity; diabetes; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein #1 of the invention. This sequence is encoded by the human-
tyrosine phosphatase gene located on chromosome 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a new human tyrosine phosphatase
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24; Mismatches
                                                                                                Human tyrosine phosphatase protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 25; Fig 2; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                          27-NOV-2001; 2001WO-EP013794.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; ABK89178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 398 AA;
                                                                                                                                                                                                                                                                                              WO200242435-A2.
                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                       Human;
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Matches
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ADD89795

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sequence represents the human cancer associated phosphatase DKF2D566K0524, which is used in the exemplification of the present
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Xue AJ, We
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                                                                                                  Sequence 398 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-DEC-2001; 2
11-DEC-2001; 2
14-MAR-2002; 2
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22-APR-2002;
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                                                            invention
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Ghosh M,
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                                                                                                                                                   Query Match
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                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       purepuacas of the present invention has Cylouscutt, immunication, antidatebric, neuroprotective, antinheumatic, antiarthritic, antiparteriosclerotic, antinheumatic, antiarthritic, antiparteriosclerotic, antinheumatory, vulnerary, antiparteriosclerotic, antinheumatory, vulnerary, synaecological and antiangiogenic activities. The cancer associated phosphatases and nucleic acids encoding the proteins are useful for visualising tumours in patients or diagnosing and treating cancer, e.g. pancreas, lung, ovarian, liver or colon cancer. The polypeptides and nucleic acids may also be used for treating hyperproliferative diseases, such as autoimmune disease, diabetes mellitus, multiple sclerosis, rheumatoid arthritis, psoriasis, atherosclerosis, infilammation, scarring, endometriosis or angiogenesis, determining the effectiveness of drugs, determining patient prognosis, or as targets for screening pharmaceutical agents that inhibit the growth or metastasis of tumour cells. The present
                                                                                                                                                                                                                                                                                                                                                                                                                    cancer associated phosphatase; enzyme; human; cancer; tumour; cytostatic; immunosuppressive; antidiabetic; neuroprotective; anticheumatic; antiarteriosclarotic; antiinflammatory; vulnerary; gynaecological; antianteriosclarotic; antiinflammatory; autoimmune disease; diabetes mellitus; multiple sclerosis; autoimmune disease; diabetes mellitus; multiple sclerosis; inflammation; scarring; refound arthritis; psoriasis; atherosclerosis; inflammation; scarring;
              New nucleic acids encoding cancer associated phosphatases, useful as targets for screening pharmaceutical agents that inhibit the growth of tumor cells, or for diagnosing and treating cancer, inflammation or
                                                                                                                FICUDOVVESAIEKNYSFDIMNIVTQMRKQRCGMIQTK 218
                                                                                                                                                                                                                                                                                                                                                                                   Human DKFZP566K0524 protein SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 10; 63pp; English.
                                                                                                                                                                                                                                                A.
                                                                                                                                                                                                                                                ADD89795 standard; protein; 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endometriosis; angiogenesis
                                                                                                                                                                                                                                                                                                                                         (first entry)
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N-PSDB; ADD89794.
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                                                                                                                                                                                                                                                                                               ADD89795;
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                                                                                                                                                                                                                                                                                  161 NREKNRYRDILPYDSTRVPLGKSKDYINASYIRIVNCGEEYFYIATQGPLLSTIDDFWQM 220
                                                                                                                                                                      VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI 121
                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang J;
Wang Z;
                                                                                                                                                                                                                                                           VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV
                                                                                NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder; contig.
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ou P, Drmanac RT,
DB 7; Length 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel protein-related contig polypeptide seguence #189.
                                                                                                                                                                                                                                                                                                                                                       218
                                                                                                                                                                                                                                                                                                                                                                                        Goodrich RW, Ren F, Zhang
                                                                                                                                                                                                                                                                                                                                                       FICVDVVFSAIEKNYSFDIMNIVTOMRKORCGMIOTK
Score 928; DB 7
Pred. No. 3e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, SEQ ID NO 2667, 1177pp; English.
                                           24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J, Wehrman T, Weng G, Z
Chen R, Xu C, Boyle BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE09123 standard; protein; 409 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002US-037238IP.
2002US-03726ISP.
2002US-00128558.
2002US-0376045P.
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2002US-0365091P.
2002US-0365384P.
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    79.08;
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                         Local Similarity 77.9 ies 169; Conservative
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Claim 20; SEQ ID NO 1172; 1177pp; English.

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                                                                                                                                                                                                                                                                                  VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV 181
                                                                                                                                                                                                                                                                                                    markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence was used in the exemplification of the invention.
                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang J;
                                                                                                                                                                         2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYPYIATQGPLPETIEDFWQM
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein (useful for identifying genetic disorders) #261.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang J, Zhao QA
ou P, Drmanac RT,
                                                                                                                        Length 409;
                                                                                                                                                 24; Indels
                                                                                                                                                                                                                                                                                                                                      FICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 218
                                                                                                                                                                                                                                                                                                                                                     Ren F, Zhany
ra G. Zhou P,
                                                                                                                     79.0%; Score 928; DB 7; 77.9%; Pred. No. 3.1e-98; ive 24; Mismatches 24;
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Boyle BJ;
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Tang YT, Asundi V, Goodii...

M Xue AJ, Wehrman T,
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11-DEC-2001; 2001US-0339453P.
14-MAR-2002; 2002US-036591P.
14-MAR-2002; 2002US-0365384P.
12-APR-2002; 2002US-0372381P.
12-APR-2002; 2002US-0372615P.
22-APR-2002; 2002US-037615P.
24-APR-2002; 2002US-0376045P.
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                                                                                                                                  Best_Local Similarity
Matches 169; Conserv
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                                                                                            Sequence 409 AA;
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                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                    VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV 181
                        The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed, as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II)
                                                                                                                                                                                                                                           2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQM
                                                                                                                                                                                                                                                                                                    VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy, forensic, food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                    Length 508;
                                                                                                                                                                                                                24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    FICUDUVESALEKNYSFDIMNIVTOMRKORCGMIQTK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                 79.0%; Score 928; DB 7; 77.9%; Pred. No. 4.3e-98;
                                                                                                                                                                                                               24; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #6033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; protein;
                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                            the invention,
                                                                                                                                                         Sequence 508 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS70229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-FEB-2002
                                                                                                                                                                                                               Matches 169;
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25-SEP-2002; 2002US-0413910P. 27-SEP-2002; 2002US-0414296P. 11-OCT-2002; 2002US-0417821P. 26-AUG-2002; 2002US-0406172P

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sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymoclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is conspiculty of (II) or to treat disease states involving (II). (II) is conspiculty of (II) and its binding partners are useful in medical imaging colspicates in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders of supplement protein expression or biological activity. The polypeptide and polymoclecide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in celectronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic; hypotensive; vasotropic; antinflammatory; antianginal; anti-HIV; antial-Ergic; antiasthmatic; immunosuppressive; antithyroid; dermatological; antidiabetic; nephrotropic; antigout; gastrointestinal; antirheumatic; antiparkinsonian; nootropic; anticonvulsant; hepatotropic; antipsoriatic; haemostatic; cytostatic; antiparasitic; antibacterial; virucide; protozozacide; fungicide; cardiovascular disease; immune system; neurological; growth; development; cell proliferation; viral; bacterial; fungal; parasitic; protozozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLENNCNVIAMITREIECGVIKCYSYMPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324 NREKNRYRDILPYDSTRVPLGKSKDYINASYIRIVNCGEEYFYIATQGPLLSTIDDFWQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79.0%; Score 928; DB 4; Length 561; 77.9%; Pred. No. 4.9e-98; ive 24; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                helminthic infection; transgenic; gene therapy; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FICUDUVESALEKNYSFDIMNIVTOMRKORCGMIQTK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human kinase and phosphatase KPP-40 protein.
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Best Local Similarity 77.99
Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 561 AA;
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25-AUG-2003; 2003WO-US026635.

04-MAR-2004.

443 181

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Gaps .,

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The invention relates to a novel isolated polypeptide which is a human kinase and phosphatase (KPP). The polypeptide of the invention demonstrates cardiovascular, antiarterisoslerotic, protectic, protectic, protectic, protectic, protectic, protectic, artiallargic, antiallargic, antidabetic, antianthritic, uropathic, aparcointestinal, neuroprotective, osteopathic, antiarthritic, uropathic, ophthalmological, antiarthritic, uropathic, ophthalmological, antiparthritic, uropathic, ophthalmological, antiparthritic, uropathic, antiparabitic, antiparterial, virucide, protectorulsant, hepatotropic, antiparatic, antiparatic, cantibacterial, virucide, protectical antiparabitic, antiparatic, antiparatic, contibacterial, virucide, protectical and fungicide activities. The kinase and phosphatase (KPP) polymoucleotides, polypeptides, agonists and antagonists may be useful for diagnosing, treating or preventing contrological disorders and viral, bacterial, fungal, parasitic, coll protection or helminthic infections. Purthermore, the molecules of the invention may be useful for creating transgence and auman collegence is that of a human collegence in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305
                                                                                                                                               Baughn MR, Richardson TW, Marquis JP, Swarnakar A, Tang YT;
Becha SD, Emerling BM, Jin P, Wilson AD, Yue H, Gietzen KJ;
Chang H, Yang YG, Lee SY, Khare R, Elliott VS, Hafalia AJA;
Chawla NK, Ramkumar J, Gururajan R, Tribouley CM, Chien D, Tran UK;
                                                                                                                                                                                                                                                                                                                             New human kinases and phosphatases, useful for diagnosing, treating or preventing atherosclerosis, hypertension, AIDS, allergy, multiple sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 NREKNRYRDILPYDSTRVPLGKSKDYINASYIRIVNCGEEYFYIATQGPLLSTIDDFWQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 VLENNSINVIAMITREIEGGIIKCYHYWPISLKKPLELKHFRVFLENYQILQYFIIRMFQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----SFNIMDIVAQMREQRSGMVOTK
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 40; 347pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 114; Conservative
                                                                                                                                                                                                                                                                        WPI; 2004-226830/21.
N-PSDB; ADK71922.
                                                                                                                  (INCY-) INCYTE CORP
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                                                                                                                                                                                                                                                                                                                                                                                                 hepatitis.
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                                                                                                                                                                                                                                       Murage J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The present sequence represents rat PTP10. The above proteins, other than ALK -7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with aboremal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and tymphomal, which modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's carine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polymucleotides encoding the proteins can be used as probes to identify and clone related sequences, to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTP04; PTP05; PTP10; SAD; ALP, ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 RVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding specific protein tyrosine phosphatases - 1 for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Markby D;
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Pred. No. 4.7e-57;
7; Mismatches 13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Page 160; 193pp; English.
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, Hui TH;
                                                                                                                                                                                                                                                                                             97US-0047222P.
97US-0049477P.
97US-0049756P.
97US-0049914P.
97US-0063595P.
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 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                Clary D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Courtneidge SA, App
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                                                                                                                                                                                                                                                                                                                                                                                               INC.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 122 AA;
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                                                                                                                                                                             WO9849317-A2
                                                                                                                                                                                                                                               27-APR-1998;
10-MAR-1999
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                                                                                                                                                                                                                                                                               28-APR-1997
                                                                                                                                                                                                                                                                                                20-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                Plowman GD,
                                                                                                                                              Rattus sp.
                                Rat PTP10
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dispoyee cells, given in the specification. The proteins are identified by selecting a bair protein from a known adipocyte marker and then performing a yeast 2-hybrid selection to isolate prey proteins encoded by members of an adipocyte colls, and proteins are designated SID members of an adipocyte colls, and proteins are designated SID comparing a polypeptide in the adipocyte cells, a recombinant host cell expressing at least one of the interacting polypeptides of the complex, selecting a modulating compound in adipocyte cells, a sID (RTM) polypeptide comprising any of the 738 amino acid sequences given in the specification (including its fragment or variant), a sID (RTM) polypucletide comprising any of the 738 nucleotide sequences given in the specification (including its fragment or variant), a vector comprising the SID (RTM) polymucleotide, a recombinant host cell comprising the Vector, a protein chip comprising the polypeptides and a recomplex, polypeptides, polymucleotides and compounds are useful for the complex, polypeptides, polymucleotides and compounds are useful for the complex of the fata, listed in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The polynucleotides are useful as probes or primers. The complex is particularly useful for identifying selected interacting domains (SID (RTM)) for screening thugs that modulate the protein interaction, thus exhibiting the therapeutic effect. The present sequence represents a SID (prey) protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ONRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as obesity or diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a complex between two interacting proteins in
                                                                                                                                                                    Human, prey, adipocyte, SID, selected interacting domain, anorectic, antidiabetic, protein-protein interaction; diabetes, yeast 2-hybrid assay; metabolic disorder, obesity.
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                                                                                                                              Human adipocyte Selected Interacting domain, SID, #319.
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46.1%; Score 541.5; DB 6;
Best Local Similarity 47.0%; Pred. No. 4.5e-53;
Matches 103; Conservative 37; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Page 208-209; 382pp; English.
ABU70688 standard; protein; 766 AA.
                                                                                                                                                                                                                                                                                                                                                                                    14-MAR-2002; 2002WO-EP003768
                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAR-2001; 2001US-0275734P
                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Daviet L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYBR-) HYBRIGENICS.
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                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                    10-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Legrain P,
                                            ABU70688;
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MVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFTVRVF 119
                        577 MIWEQKSTVIAMMIQEVEGEKİKCORYWPNILGKTIMVSNRLRLALVRMQQLKGFVVRAM 636
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                                                          120 QIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRT
                                                                           Yamamoto J;
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                                                                                                                                                                                                                                                                                                                                         Human; protein kinase; protein phosphatase; signal transduction.
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Best Local Similarity 47.0%; Pred. No. 9.2e-53;
Matches 103; Conservative 37; Mismatches 78; Indels
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Otsuki
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                                                                                                                                        hikawa T, Hayashi K, S
Wakamatsu A, Nagai K,
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                                                                                                                                                                                                                                                                                                                 Amino acid sequence of a human protein.
                                                                                                                                                                                                                            AAG67637 standard; protein; 1267 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUL-1999; 99JP-00248036.
18-OCT-1999; 99US-0159590P.
11-JAN-2000; 2000JP-00118776.
17-EB-2000; 2000US-018322P.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-001899.
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Nezu J;
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Senoo C,
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1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ

Gaps

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1078 MIWEQKSTVIAMMIQEVEGEKİKCORYMPNILGKITMVSNRLRLALVRMQQLKGFVVRAM 1137
                                                                                               61 MVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFTVRVF 119
                                                                        120 QIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRKSHITGPLLVHCSAGVGRT 179
                                                                                                                                                                           GVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 218
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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1, 2004, 12:07:39; Search time 85.8421 Seconds (without alignments) 1561.731 Million cell updates/sec US-09-095-478A-6_COPY_225_457 1253 Title: Perfect score:

1 QNRDKNRYRDILPYDSTRVP......MIQTKEQYQFCYEIVLEVLQ Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1825181 Total number of hits satisfying chosen parameters:

1825181 seqs, 575374646 residues

Searched:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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37	1.1												
		473.5	473.5	472.5	472.5	472.5	471.5	471.5	471	471	470.5	470	469.5

ALIGNMENTS

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the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
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                                                                01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Protein-tyrosine-phosphatase (EC 3.1.3.48) (Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4921505B14
product.protein tyrosine phosphatase, non-receptor type 20, full
                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                              TISSUE-Testis;
MEDLINE=98070510; PubMed=9407093;
Obsugi M., Kuramochi S., Matsuda S., Yamamoto T.;
"Molecular cloning and characterization of a novel cytoplasmic protein-tyrosine phosphatase that is specifically expressed in spermatocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/60; TISSUB-Testis;
MEDLINE=99279253; PubMed=10349636;
Carninol P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                    426 AA.
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                                    PRT;
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STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851;
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STRAIN=CS7BL/6J; TISSUE=Testis;
The FANTOM Consortium,
                                  PRELIMINARY;
                                                                                                                                                                                                         Mus musculus (Mouse)
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                                                                                                                                                                            insert sequence).
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                                                                                                                                                                                           Name=Ptpn20;
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RESULT 1
055082
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398 AA

PRT;

PRELIMINARY;

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SEQUENCE
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Antuda S., Furuno M., Hangaki T., Hara A., Hashizume W., Fukuda S., Furuno M., Hangaki T., Hara A., Hashizume W., Arayashida K., Hayatsu N., Hiramoto K., Hiracka T., Hirozane T., Antoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Mirhara C., Matuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Togaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, D64141; BAA2376:1; -.

REMBL, MC029493; BAC26476:1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 ONRDKNRYRDÍLÞYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATOGPLÞETIEDFWO 247
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prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                               STRAIN=C57BL/61); TISSUB=Testis; MEDLINE=20530913; PubMed=11076861; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Harama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kabhinagi K., Voneda Y., Ishikawa T., Ozawa M., Olara B., Watsuhiwagi K., Voneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Norda Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Firks integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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R MGD; MGI:119629; Prpn20.

R GO; GO:0016787; F:hydrolase activity; IEA.

R GO; GO:000472; F:protein tyrosine phosphatase activity; IEA.

R GO; GO:000472; F:receptor activity; IEA.

R GO; GO:000472; F:receptor activity; IEA.

R GO; GO:000470; P:protein amino acid dephosphorylation; IEA.

R InterPro; IPR0004242; TYr_PP.

R InterPro; IPR0004242; TYr_PP.

R FAUNTS; PR00700; PRTYPHPHTASE.

R PRINTS; PR00700; PRTYPHPHTASE.

SMART; SM00194; PTPC; I.

R PROSITE; PS00056; TYR_PHOSPHATASE_1; I.

PROSITE; PS50056; TYR_PHOSPHATASE_2; I.
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Matches 233; Conservative
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A Ansorge W. Wirkner U., Mewes H.W., Gassenhuber J., Wiemann S.;
Aubmitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL050040; CAB42248.1; -.
EMBL; AL050040; CAB42248.1; -.
ROG, GO:0016737; Frydzolase activity; IEA.
GO; GO:00064725; Frydzolase activity; IEA.
GO; GO:0006470; Protein tyrosine phosphatase activity; IEA.
GO; GO:0006470; Protein amino acid dephosphorylation; IEA.
INTEPRO; IPR000242; TYR_Phosphatase.
R InterPro; IPR000242; TYR_PP.
R Ffam; PF00102; Y_phosphatase; 1.
R RNART; RM00194; PTPC; 1.
R RNART; RM00194; PTPC; 1.
R RNSITE; PS00383; TYR_PHOSPHATASE_1; 1.
R RNSITE; PS50055; TYR_PHOSPHATASE_2; 1.
W Hydrolase; Hypothetical protein.
TYRON_TERR.
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Bukaryota Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria, Cetartiodactyla, Ruminantia, Pecora; Bovidae,
Bovinae, Bos.
                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Vega Q.C., Walton K.M., Dixon J.E.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 5 PDZ/DHR domains.
EMBL; U20807; AAA73516.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                398 AA; 45690 MW; 857AAD03747870A2 CRC64;
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Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein DKFZp566K0524 (Fragment).
Name=DKFZp566K0524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.4%; Score 995; DB 2; 78.0%; Pred. No. 1.2e-87; iive 26; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 2484 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 78.03
Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 QIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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064512, 061494; 062135; 064499;
29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
Protein tyrosine phosphatase, non-receptor type 13 (EC 3.1.3.48)
(Protein tyrosine phosphatase PTP-BL) (Protein tyrosine phosphatase RIP)
Name=Ptpn13; Synonyms=Ptp14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2415 GTLICIDVVLGLISQDLEFDISDLYRCMRLQRHGMYQTBDQYIFCYQVILYYL 2467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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HSSP; Q64512; 1CM1.

G0; G0:0005856; C:cytoskeleton; IEA.

G0; G0:0005817; F:hydrolase activity; IEA.

G0; G0:0005515; F:protein binding; IEA.

G0; G0:00064725; F:protein tyrosine phosphatase activity; IEA.

G0; G0:0006470; P:protein mino acid dephosphorylation; IEA.

InterPro; IPR001099; Band 4.1.

InterPro; IPR011099; Kinase_like.

InterPro; IPR011099; Kinase_like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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48.9%; Pred. No. 3.5e-49;
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PROSITE; PS00661; FERM_2; PALSE_NEG.
PROSITE; PS00651; FERM_3;
PROSITE; PS00106; PDZ; 5:
PROSITE; PS00106; PDZ; 5:
PROSITE; PS00106; PYR; PHOSPHATASE 1; FALSE_NEG.
PROSITE; PS001065; TYR_PHOSPHATASE_2; 1.
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                                                                                                                                                                                                                                                                                                 Interpro; IPR001478; PDZ.
Interpro; IPR011036; PH related.
Interpro; IPR00387; TYR phosphatase.
Interpro; IPR000242; Tyr PP.
Pfam; PP00595; PDZ; 5.
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SMART; SM00750; KIND; 1.
SMART; SM00228; PDZ; 5.
SMART; SM00194; PTPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2484 AA;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus

Mus musculus (Mouse)

NCBI_TaxID=10090;

SEQUENCE FROM N.A. STRAIN=C57BL/6; TISSUE=Skin; MEDLINE=96340953; PubMed=8749712;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tyrosine + phosphate.

-- SUBUNIT: Binds PLEKHA1 and PLEKHA2 through its first PDZ domain (By similarity). Interacts with TRIPS of TRRESFG (Fas receptor) through its second PDZ domain. Interacts with the C-terminal SVP motif of NGTR through its second and fourth PDZ domains. Interacts with the LIM domain of PDIIMH through its second and fourth PDZ domains.
-- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-- TISSUE SPECIFICITY: Expressed predominantly in kidney and, to a lesser extent, in lung, heart, brain and testis.
-- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
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Hendriks W., Schepens J., Baechner D., Rijss J., Zeeuwen P., Zechner U., Hameister H., Wieringa B.; "Molecular cloning of a mouse epithelial protein-tyrosine phosphatase with similarities to submembranous proteins."; J. Cell. Biochem. 59:418-430(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: Regulates negatively FAS-induced apoptosis and NGFR-mediated pro-apoptotic signaling.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                            "Characterization of a protein tyrosine phosphatase (RIP) expressed a very early stage of differentiation in both mouse erythroleukemia and embryonal carcinoma cells.";
FEBS Lett. 358:233-239(1995).
                                                                                                                                                                                                                                                                                                                                                                                                          Sawada M., Ogata M., Fujino Y., Hamaoka T., "cDNA cloning of a novel protein tyrosine phosphatase with homology cytoskeletal protein 4.1 and its expression in T-lineage cells."; Biochem. Biophys. Res. Commun. 203:479-484(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=BALB/c; TISSUE=Brain; MEDLINE=95134212; PubMed=7832766; Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B.; "A novel receptor-type protein tyrosine phosphatase with a single catalytic domain is specifically expressed in mouse brain."; Biochem. J. 305:499-504(1995).
                                                                                                                                                                  MEDIJNE=91145716; PubMed=7843407;
Chida D., Kume T., Mukouyama Y., Tabata S., Nomura N., Thomas M.,
Watanabe T., Oishi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 1 FERM domain.
-!- SIMILARITY: Contains 5 PDZ/DHR domains.
                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1105-2452 FROM N.A. STRAIN-CB.17 SCID; TISSUE=Thymus; MEDLINE=94354845; PubMed=8074693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol, Cell 9:671-683(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 2267-2373 FROM N.A.
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EMBL; D83966; BAA12158.1; -.
EMBL; D28529; BAA05885.1; -.
EMBL; Z23059; CAA80594.1; -.
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PIR; PT0635; PT0696.
PIR; PT0649; PT0712.
PIR; S40290; S40290.
PIR; S71625; PT085.
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                     STRAIN=DBA/2;
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118 VPQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVG 177
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16-0CT-2004 (Rel. 40, Last sequence update)
01-0CT-2004 (Rel. 45, Last sequence update)
protein tyrosine phosphatase, non-receptor type 13 (EC 3.1.3.48)
(Protein-tyrosine phosphatase 1E) (PTP-EL) (hPTPEI) (PTP-EAS)
(Protein-tyrosine phosphatase PTPLI) (FSS-associated protein-tyrosine phosphatase 1) (FSS-associated protein-tyrosine
2380 GRSGTLICIDVVLGLISQDLEFDISDLVRCWRLQRHGMVQTBGQYVFCYQVILYVL 2435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 MVLENNCNVIAMITREJECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQY---FTVR
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                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Q12933; Q15159; Q15263; Q15264; Q15265; Q15674; Q16826; Q8IWH7;
Q9NYN9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Lisovsky M.Y., Itoh K., Sokol S.Y.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AY327257, AAR9/1566.1;
NON_TER 2500 2500
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                                                                                                                                                                                                                                                    01-OCT-2004 (TrEMBLrel. 28, Created)
01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Frizzled-8 associated multidomain protein (Fragment)
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                                                                                                                                                                                           2500
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TISSUE=Breast carcinoma;
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Best Local Similarity
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HIRNSNCAPSFSN -> TSGTASRAFVSY (in Ref.
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270332 MW; 53396F27AE2582F2 CRC64;
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PROSITE; PS00661; PERM 1; FALSE NEG.

PROSITE; PS00661; PERM 3; 1.

PROSITE; PS00057; PERM 3; 1.

PROSITE; PS00106; PDZ, 5.

PROSITE; PS00106; PDZ, 5.

PROSITE; PS00106; PDZ, 5.

PROSITE; PS00106; TYR_PHOSPHATASE_1; FALSE_NEG.

PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.

PROSITE; PS50055; TYR_PHOSPHATASE_2; 1.

PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.

PROSITE; PS50056; TYR_PHOSPHATASE_PTP; 1.

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InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000343; Tyr_PP.
Pfam; PF001973; Band 41; I.
Pfam; PF00105; PDZ, 5.
Pfam; PF00105; PAND41.
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SMART; SM00228; PDZ; 5.
SMART; SM00194; PTPc; 1.
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MGD; MGI:103293; Ptpn13
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CALSINGE=22388257; PubWed=12477932; DOI=10.1073/pnas.242603899;
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A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
CALSTONE R.F., Ordan H., Moore T., Max S.L., Wang J., Hsheh F.,
CALSTONE R.F., Moran T.B., Toshiyuki S., Carninci P., Prange C.,
CALSTONE R.F., McCarnan R.J., Abramson R.D., Mullahy S.J.,
CARAN S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
CARAN S.S., McCarnan P.J., McKernan R.J., Marmanne P.H.,
CALSTONE R. K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
CALSTONE R. K., Touchman J.W., Green E.D., Dickson M.C.,
CALSTONE R. M., Touchman J.W., Green E.D., Dickson M.C.,
CALSTONE R. M., Touchman J.W., Green E.D., Dickson M.C.,
CALTHWOOD AND M., Krzywinski M.I., Skalska U., Smailus D.E.,
CALSTONE R. M., Marra M.A.,
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a membrane-binding ofmain and GLGF repeats.";
FEBS Lett. 337:200-206(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutthy K.K., Clark K., Fortin Y., Shen S.-H., Banville D.; "ZRP-1, a zyxin-related protein, interacts with the second PDZ domain of the cytosolic protein tyrosine phosphatase hPTPIE."; J. Biol. Chem. 274:20679-20687(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=9523528; PubMed=7536343;
Sato T., Irie S., Kitada S., Reed J.C.;
"FAP-1: a protein tyrosine phosphatase that associates with Fas.";
Science 268:411-415(1955).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERACTION WITH NGFR.
MEDLINE=20012928; PubMed=10544233;
Irie S., Hachiya T., Rablzadeh S., Maruyama W., Mukai J., Li Y.,
Reed J.C., Bredesen D.E., Sato T.A.,
"Functional interaction of Fas-associated phosphatase-1 (FAP-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang H.Y.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1323-1821 FROM N.A.
Irie S., Hachiya T., Sato T.A.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                       FROM N.A., AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1279-1883 FROM N.A. (ISOFORM 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 269:24082-24089(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99329089; PubMed=10400701;
                                                                                                             MEDLINE=94116679; PubMed=8287977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1216-2490 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1323-1922 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERACTION WITH TRIP6.
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Pancreas;
Wang H.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc.
ARENE BARKEREN BEREN BEREN BEREN BARKEREN BARKEREN BEREN REN BEREN BEREN BEREN BEREN BEREN BEREN BEREN BEREN BEREN BER BEREN BEREN BEREN BEREN BEREN BEREN BEREN BEREN BEREN BEREN BER BEREN BEREN BEREN BEREN BEREN BEREN BEREN BEREN BEREN BEREN BER
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"Functional interaction of Fas-associated phosphatase-1 (FAP-1) with p75 (NTR) and their effect on NF-kappaB activation.";

[10] INTERACTION WITH PLEKHA1 AND PLEKHA2.

PEBS Lett. 460:191-198(1999)

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                                                                                                                                                                                  Kozlov G., Gehring K., Ekiel I.;
"Solution structure of the PDZ2 domain from human phosphatase hPTP1E
and its interactions with C-terminal peptides from the Fas receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of PDLIM4 through its second and fourth PDZ domains. Binds PLEKHAl and PLEKHA2 through its first PDZ domain.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isoid=Q12923-4; Sequence=VSP_007921;
Note=May be due to a competing donnor splice site;
TISSUE SPECIFICITY: Present in most tissues with the exception of
the liver and skeletal muscle. Most abundant in lung, kidney and
fetal brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tyrosine + phosphate.
-!- SUBDANT: Interacts with TRIP6 and TNRRSF6 (Fas receptor) through its second PDZ domain. Interacts with the C-terminal SVP motif of NGFR through its third PDZ domain. Interacts with the LIM domain
                                                                                                                                                                                                                                                                                                        GUANINE NUCLEOTIDE EXCHANGE FACTOR RA-GEP-2.
MEDLINE=22090786; PubMed=12095257; DOI=10.1016/S0022-2836(02)00544-2; Kozlov G., Banville D., Gehring K., Ekiel I.;
"Solution structure of the PDZ2 domain from cytosolic human phosphatase hPTPLE complexed with a peptide reveals contribution of the beta2-beta3 loop to PDZ domain-ligand interactions."; Mol. Biol. 320:813-820(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yoshida S., Harada H., Nagai H., Fukino K., Teramoto A., Emi M.;
"Head-to-head juxtaposition of Fas-associated phosphatase-1 (FAP-1)
and c-Jun NH2-terminal kinase 3 (JNK3) genes: genomic structure and
seven polymorphisms of the FAP-1 gene.";
J. Hum. Genet. 47:614-619(2002).
-!- FUNCTION: Regulates negatively FAS-induced apoptosis and NGFR-
mediated pro-apoptotic signaling.
-!- CATALYIIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR OF 1361-1456 IN COMPLEX WITH THE C-TERMINUS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Non-receptor class subfamily. SIMILARITY: Contains 1 FERM domain. SIMILARITY: Contains 5 PDZ/DHR domains.
                                                                                                                        STRUCTURE BY NMR OF 1361-1456 UNCOMPLEXED AND IN COMPLEX WITH THE
               Kimber W.A., Deak M., Prescott A.R., Alessi D.R.;
"Interaction of the protein tyrosine phosphatase PTPL1 with the
PtdIns (3.4) P2-binding adaptor protein TAPP1.";
Biochem. J. 376:525-555(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS PRO-1419 AND MET-1522.
MEDLINE=223233362; PubMed=12436199; DOI=10.1007/s100380200094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=3;
IsoId=Q12923-3; Sequence=VSP_000497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q12923-2; Sequence=VSP_000496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=Q12923-1; Sequence=Displayed;
                                                                                                                                            C-TERMINUS OF TNFRSF6.
MEDLINE=20170882; PubMed=10704206;
                                                                                                                                                                                                                                                    Biochemistry 39:2572-2580(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , D21209; BAA04750.1; -...
D21210; BAA04751.1; -...
D21211; BAA04751.1; -...
X80289; CAA56563.1; -...
X79676; CAA56124.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U12128; AAB60339.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
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PRINTS; PR00935; BAND41.
PRINTS; PR00661; ERMFAMILY.
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00295; B41; 1.
SMART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00228; PDZ; 1.
SMART; SM00194; PTPc; 1.
SMART; SM00404; PTPc_motif; 1.
                                                                                                                                                                                                                                                                                              Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 43.5
Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        TISSUE=Oocytes;
                                                                                                                                                                                                                                                                                      initiative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 QIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 MVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFTVRVF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Oocytes;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                                                                                         MIM; 600267;

R GO; GO:0004725; F:protein-tyrosine-phosphatase activity; TAS.

R GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.

R InterPro; IPR000299; Band 4.1.

R InterPro; IPR0004065; FERM.

R InterPro; IPR001478; PDZ.

R InterPro; IPR001478; PDZ.

R InterPro; IPR001478; PDZ.

R InterPro; IPR001478; PDZ.

R InterPro; IPR000387; TYR phosphatase.

R InterPro; IPR000342; TYR PP.

R Pfam; PF00373; Band 41; I.

R Pfam; PF00595; PDZ, 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 GVFICVDVVFSAIBKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVL
                                                                                                                                                                                                                                                                                                                                                                                        Length 2485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                         47.3%; Score 592.5; DB 1; 47.6%; Pred. No. 1e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                  80;
                                                                                                                                                                                                                                                                         Pram, Pr00102, Y_phosphatase; 1.
PRINTS; PR001035; BAND41.
PRINTS; PR00700; PRTYPHPHTASE.
PROSTITE; PS00660; FERM 1; FALSE_NEG.
PROSTITE; PS00661; FERM 2; FALSE_NEG.
PROSTITE; PS00061; FERM 2; FALSE_NEG.
PROSTITE; PS00106; PDZ; 5.
PROSTITE; PS00106; PDZ; 5.
PROSTITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                  41; Mismatches
  EMBL; L34583; AAC41755.1; -.
EMBL; BC333; AAF63474.1; -.
EMBL; BC039610; AAH39610.1; ALT_TERM.
PIR; A54971; A54971.
PIR; I67629; I67629.
PIR; I67629; I67630.
PDB; 1D5G; NMR; A=1361-1456.
PDB; 1D7X; NMR; A=1361-1456.
PDB; 3PDZ; NMR; A=1361-1456.
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 47.6%
Matches 111; Conservative
                                                                                                                 Genew; HGNC:9646; PTPN13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8355;
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodiguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,
Andriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
Andriguez M.C., Salailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
Andriguez M.D., Balalysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYI-----RIVNHEEEYFYIATQGPLPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 920;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein S., Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50106; PDZ; 1.
PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE 2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE PTP; 1.
Hydrolase; Hypothetical protein.
SEQUENCE 920 Aa; 105109 MW; 8F0BB89C359CD41E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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43.5%; Pred. No. 2.9e-40;
iive 33; Mismatches 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 PDZ/DHR domain.
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InterPro; IPR000299; Band 4.1.
InterPro; IPR000798; Earlad/moesin.
InterPro; IPR000198; ERM.
InterPro; IPR001478; PDZ.
InterPro; IPR0011036; PH related.
InterPro; IPR000395; FPFC_motif.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; TYR_PP.
Ffam, PP00375; Band 41; I.
Pfam, PP00375; PDZ; I.
Pfam, PP00102; Y_phosphatase; I.
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PROSITE; PS50057; FERM 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22341132; PubMed=12454917;
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Yachi A.;
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790 YVFREMLLIDIETGDEFPIIHLQYVAWPDHGVPDDSSDFLEFATYVRQKRMENQPVLVHC 849
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                                                          SAGVGRIGVFICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEV
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
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01-MAY-1992 (Rel. 22, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Protein tyrosine phosphatase, non-receptor type 3 (EC 3.1.3.48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC033716; AAH33716.1; -.
GO, GO:0016787; F:hydrolase activity; IEA.
GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
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Last annotation update)
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InterPro; IPR000242; TYR PP.
Pfam; PR00102; Y_phosphatase; 1.
PRINTS: PR00700; PRTYPHPHTASE.
SMART; SM00194; PTPC; 1.
PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
PROSITE; PS0056; TYR_PHOSPHATASE 2; 1.
PROSITE; PS0056; TYR_PHOSPHATASE 2; 1.
PROSITE; PS0056; TYR_PHOSPHATASE 2; 1.
PROSITE; PS0056; TYR_PHOSPHATASE 2; 1.
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                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein (Fragment).
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                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                              Yang Q., Tonks N.K.;
"Isolation of a cDNA clone encoding a human protein-tyrosine
phosphatase with homology to the cytoskeletal-associated proteins band
4.1, ezrin, and talin.";
Proc. Natl. Acad. Sci. U.S.A. 88:5949-5953(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytoskeleton.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tyrosine + phosphate.
--- SUBCELLULAR LOCATION: Cytoplasmic.
--- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamins.
--- SIMILARITY: Contains 1 FREM domain.
--- SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-2022.,
MEDLINE-2022.,
MEDLINE 2., Hinoda Y., Itoh F., Takekawa M., Tsujisaki M., Adachi
Imai K., Yachi A.;
"cDNA cloning of new protein tyrosine phosphatases in the human
                                                                                                       Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
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MIM; 176877; ...

GO; GO:0006470; P:protein-tyrosine-phosphatase activity; TAS.

GO; GO:0006470; P:protein-mino acid dephosphorylation; TAS.

R InterPro; IPR000299; Bz/rad/moesin.

R InterPro; IPR001478; PDZ.

R InterPro; IPR0010478; PDZ.

R InterPro; IPR000542; TYP. PP.

R Pfam; PF00373; Band_41; I.

R Pfam; PF00595; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ikuta S., Itoh F., Hinoda Y., Toyota M., Makiguchi Y., Imai K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTPH1 mRNA in human hepatocellular carcinoma.";
J. Gastroenterol. 29:727-732(1994).
-!- FUNCTION: May act at junctions between the membrane and
(Protein-tyrosine phosphatase H1) (PTP-H1).
Name=PTPN3; Synonyms=PTPH1;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 899-913 FROM N.A.
MEDLINE=95179278; PubMed=7874267;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=91296738; PubMed=1648725;
Yang Q., Tonks N.K.;
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                                                                                                    Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumour Biol. 13:180-186(1992)
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HSSP; P18031; 1C88.
Genew; HGNC:9655; PTPN3.
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SMART; SM00228; PDZ; 1.
SMART; SM00194; PTPc; 1.
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389 NPAYIFRKWILINQEKNESRQLIQIQYTAWPDHGVPDDSSDFLDFVCHVRDQRAGKEEPI 848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 --YFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVR--KSHITGPL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIV 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Fetal brain;
MEDLINE=96102179; PubMed=8524829;
Pulido R., Serra-Pages C., Tang M., Streuli M.;
"The LAR/FTP delta/FTP sigma subfamily of transmembrane protein-tyrosine-phosphatases: multiple human LAR, PTP delta, and PTP sigma isoforms are expressed in a tissue-specific manner and associate with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ONRDKNRYRDILPYDSTRVPLGKNKDYINASYIR-----IVNHEEBYFYIATQGPLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      013332; 075255; 075870; 015718; 016341;
110-0CT-2003 (Rel. 42, Created)
01-0CT-2004 (Rel. 45, Last sequence update)
01-0CT-2004 (Rel. 45, Last sequence update)
Receptor-type protein-tyrosine phosphatase S precursor (EC 3.1.3.48)
(R-PTP-S) (Protein-tyrosine phosphatase sigma) (R-PTP-sigma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.4%; Score 493.5; DB 2; Length 926; 41.2%; Pred. No. 1.1e-38; ive 43; Mismatches 80; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   926 AA; 105713 MW; A344DAD4FF7E2AE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1948 AA.
                                                                                                                                                                                                                                                                                                                        SMART; SM00194; PTPC; 1.

SMOAITE, PS00660; FERM 1; UNKNOWN 1.

PROSITE; PS0061; FERM 2; 1.

PROSITE; PS00057; FERM 3; 1.

PROSITE; PS00036; PDZ; 1.

PROSITE; PS00036; TYR PHOSPHATASE 1; 1.

PROSITE; PS00056; TYR PHOSPHATASE 2; 1.

PROSITE; PS50056; TYR PHOSPHATASE 2; 1.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000798; Ez/rad/moesin.
InterPro; IPR0004065; FERM.
InterPro; IPR001470; PDZ.
InterPro; IPR001470; PDZ.
InterPro; IPR001387; TYR_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000387; TYR_PP.
Ffam; PF00102; Y_phosphatase; 1.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00102; Y_phosphatase; 1.
PRINTS; PR00102; Y_phosphatase; 1.
PRINTS; PR00103; BAND41.
PRINTS; PR00700; PRTYPHPHTASE.
SMART; SM00228; PDZ; 1.
SMART; SM00228; PDZ; 1.
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LKVYE 913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase.
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PTNS_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                         669 QNLDKNRYKDVLPYDTTRVLLQGNEDYINASYVNMEIPAANLVNK-----YIATQGPLPH 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 TIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEH--FSVFLETFHVT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 QYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHI-TGPLLV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 HCSAGVGRIGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLE 230
                                                                                                                                                                                                                                                                                                                                                                                                   1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYI-----RIVNHEEEYFYIATQGPLPE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, P11171; 1GG3.
MGD; MG1:1099792; Ptpn4.
GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. . .; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             724 TCAQFWQVVWDQKLSLIVMLTTLTERGRIKCHQYWP---DPPDVMNHGGFHIQCQSEDCT
                                                                                                                                                                                                                                                                                                                                                            18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular cloning and characterization of a protein tyrosine phosphatase enriched in testis, a putative murine homologue of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
    PROSITE; PS00660; FERM 1; 1.
PROSITE; PS00661; FERM 2; 1.
PROSITE; PS00057; FERM 3; 1.
PROSITE; PS00183; TYR PHOSPHATASE 1; 1.
PROSITE; PS00183; TYR PHOSPHATASE 2; 1.
PROSITE; PS00185; TYR PHOSPHATASE 2; 1.
CYLOSKeleton; Hydrolase; Protein Phosphatase; Structural protein.
                                                                                                                                                                                                                                  Phosphocysteine intermediate (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUBETeatis;
MEDLINE=20510023; PubMed=11054567;
Park K.W., Lee B.J., Lee S.H., Lee J.E., Choi E.Y., Kim B.J., Hwang R., Park K.A., Baik J.H.;
                                                                                                                                                                                                                                                                                                               Length 913;
                                                                                                                                                                                                                   Protein-tyrosine phosphatase
                                                                                                                                                                                                                                                                                                                                                          85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIŜSUE=Testis;
Choi E.-Y., Park K.-W., Lee E.-J., Baik J.-H.;
Submittad (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
EMBL; AF106702; AAD22773.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, Created)
1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last amnotation update)
Testis-enriched protein tyrosine phosphatase.
                                                                                                                                                                                                                                                                                                                 39.8%; Score 499; DB 1;
42.0%; Pred. No. 3.3e-39;
tive 38; Mismatches 85
                                                                                                                                                                             FERM.
                                                                                                                                                                                                                                                                             913 AA; 104029 MW;
                                                                                                                                                                                                                                                                                                               Query Match 39.8%;
Best Local Similarity 42.0%
Matches 102; Conservative
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the Swiss Institute of Bioinformatics and the EMBL outstation
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   Carbence From N.B.

Bubmed=15057824; DOI=10.1038/nature02399;

Grimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,

A mardin J.E., Hablsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,

Amerts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,

A merts A., Altherr M., Caoile C., Chan Y.M., Christensen M.,

Caenepeel S., Copeland A., Dalin E., Dehal P., Densy M., Detter J.C.,

B.Scobar J., Flowers D., Fctopulos D., Garcia C., Georgescu A.M.,

Glavina T., Gomez M., Gonzales E., Groza M., Hammon N., Hawkins T.,

Haydu L., Ho I., Huang W., Israni S., Jett J., Kadner K., Kimball H.,

Kobayashi A., Larionov V., Leem S., Jett J., Radner K., Kimball H.,

Robison K., Nolan M., Ovcharenko I., Pitluck S., Pollard M.,

Rodriguez A., Rogers S., Salamov A., Salazar A., Shith D.,

Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,

Vo N., Wagner M., Wheeler J., Wu K., Xie G., Yang J., Dubchak I.,

Furey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,

Rubin E.M., Lucas S.M.;

Rubin E.M., Richadson P., Stubbs L., Rokhsar D.S., Myers R.M.,

Rubin E.M., Lucas S.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98288299; PubMed=9624133;
Serrar-Pages C., Medley Q.G., Tang M., Hart A., Streuli M.;
Serrar-Pages C., Medley Q.G., Tang M., Hart A., Streuli M.;
Liptins, a family of LAR transmembrane protein-tyrosine phosphatase-interacting proteins ";
J. Biol. Chem. 273:15611-15620(1998).

-I. FUNCTION: Interacts with LAR-interacting protein LIP.1.
-I. CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                  MEDLINE=96255038; PubMed=8992885;
Endo N., Rutledge S.J., Opas B.E., Vogel R., Rodan G.A., Schmidt A.;
"Human protein tyrosine phosphatase-sigma: alternative splicing and
inhibition by bisphosphonates.";
J. Bone Miner. Res. 11:535-543(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92119637; PubMed=1370651; Adachi M., Sekiya M., Arimura Y., Takekawa M., Itoh F., Hinoda Y., Imai K., Yachi A.; A., "Protein-tyrosine phosphatase expression in pre-B cell NALM-6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q13332-3; Sequence=VSP_050022, VSP_050026, VSP_050027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the protein-tyrosine phosphatase family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=PTPS-F4-7;
IsoId=Q13332-5; Sequence=VSP 050023, VSP 050025;
TISSUE SPECIFICITY: Detected in all tissues tested except for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor class 2A subfamily.
--- SIMILARITY: Contains 8 fibronectin type III domains.
--- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
--- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The DNA sequence and biology of human chromosome 19.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tyrosine + phosphate.
SUBUNIT: Interacts with PPFIA1, PPFIA2 and PPFIA3.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
the LAR-interacting protein LIP.1.";
Proc. Natl. Acad. Sci. U.S.A. 92:11686-11690(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=PTPS-MEA;
IsoId=Q13332-2; Sequence=VSP_050021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q13332-4; Sequence=VSP_050024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 428:529-535(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            placenta and liver.
                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=PTPS-MEB;
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=PTPS-MEC;
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                        .; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAILUS, PROGUCO, FAILE FAILUSE.
SMART; SMO0660; FN3, 8.
SMART; SMO0184; PTPC; 2.
SMART; SMO0194; PTPC; 2.
PROSITE; PSSO835; FN3 LIG LIKE; 3.
PROSITE; PSSO835; TYR_PHOSPHATASE 1; 2.
PROSITE; PSSO056; TYR_PHOSPHATASE 2; 2.
ALCETALIS, PSSO055; TYR_PHOSPHATASE 2; 2.
ALCETALIS, PSSO055; TYR_PHOSPHATASE 2; 2.
ALCETALIS, PSSO055; TYR_PHOSPHATASE 2; 2.
ALCETALIS, PSSO055; TYR_PHOSPHATASE 2; 2.
ALCETALIS, PSSO055; TYR_PHOSPHATASE 3.
ALCETALIS, PSSO055; TYR_PHOSPHATASE 3.
ALCETALIS, PSSO055; TYR_PHOSPHATASE 3.
ALCETALIS, PSSO055; TYR_PHOSPHATASE; SIGNAL; SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                     R MIM; 601576; -

GO; GO:0005887; C:integral to plasma membrane; TAS.

R GO; GO:0005801; F:transmembrane receptor protein tyrosine pho. . .;

R InterPro; IPR003962; FNIII subd.

R InterPro; IPR003961; FN III.

R InterPro; IPR008957; FW III-like.

R InterPro; IPR001959; Ig-like.

R InterPro; IPR001958; Ig-like.

R InterPro; IPR001958; Ig-like.

R InterPro; IPR000242; Tyr_PP.

R Ffam; PF000041; fin3; 8.

R Ffam; PF001004; En3; 8.

R Pfam; PF001001; Y_phosphatase; 2.

R PRINTS; PR001001; Y_phosphatase; 2.

R PRINTS; PR001001; PRTYPHPHTASE.
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N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphocysteine intermediate (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor-type protein-tyrosine phosphatase S. Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Missing (in isoform PTPS-MEA).
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Protein-tyrosine phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potential.
Cytoplasmic (Potential).
Ig-like C2-type 1.
Ig-like C2-type 2.
Ig-like C2-type 3.
Ig-like C2-type 1.
Ig-like C2-type 1.
Ig-like C2-type 1.
Ig-like C2-type 1.
Ig-like C2-type 1.
Ig-like C2-type 1.
Fibronectin type-III 2.
Fibronectin type-III 5.
Fibronectin type-III 6.
Fibronectin type-III 6.
Fibronectin type-III 6.
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                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity)
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                                                                                                                                                                     EMBL, U35234; AACS0299.1; -...
EMBL, AC0317, AACC937.1; -...
EMBL, AC065338; AAC2832.1; -...
EMBL, AC065338; AAC27825.1; -...
EMBL, S78080; AAB21146.2; -...
HSSP; P10586; 11AR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263
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"Two receptor tyrosine phosphatases of the LAR family are expressed in
             the developing leech by specific central neurons as well as select peripheral neurons, muscles, and other cells.";

10. Neurosci. 18:2991-3002(1998).

11. Neurosci. 18:2991-3002(1998).

12. Neurosci. 18:2991-3002(1998).

13. EMBL; AF017083; AAB91460.1; -.

13. EMBL; AF017083; AAB91460.1; -.

13. Rissp; P10586; ILAR.

13. Rissp; P10586; ILAR.

13. GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.

13. GO; GO:0004725; F:protein amino acid dephosphorylation; IEA.

13. Ricerpro; IPR003962; FnIII_subd.

13. Ricerpro; IPR003967; FN III-like.

13. Ricerpro; IPR003967; FN III-like.

13. Ricerpro; IPR003967; TN III-like.

14. Ricerpro; IPR003967; TN III-like.

15. Ricerpro; IPR003967; TN III-like.

16. Ricerpro; IPR003967; TN III-like.

17. Ricerpro; IPR003967; TN III-like.

18. Ricerpro; IPR003967; TN III-like.

19. Ricerpro; IPR003967; TN III-like.

10. Ricerpro; IPR003967; TN III-like.

10. Ricerpro; IPR003967; TN III-like.

10. Ricerpro; IPR003967; TN III-like.

10. Ricerpro; IPR003967; TN III-like.

10. Ricerpro; IPR003967; TN III-like.

10. Ricerpro; IPR003967; TN III-like.

10. Ricerpro; IPR003967; TN III-like.

10. Ricerpro; IPR003967; TN III-like.

10. Ricerpro; IPR003967; TN III-like.

10. Ricerpro; IPR003967; TN III-like.

10. Ricerpro; IPR003967; TN III-like.

10. Ricerpro; IPR003967; TN III-like.

10. Ricerpro; IPR003967; TN III-like.

10. Ricerpro; IPR003967; TN III-like.

10. Ricerpro; IPR003967; TN III-like.

10. Ricerpro; IPR003967; TN III-like.

10. Ricerpro; IPR003967; TN III-like.

10. Ricerpro; IPR003967; TN III-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSAGVGRIGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEV
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;

Blasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;

Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.

NCBI_TaxID=86373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2051;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Receptor. _
SEOUENCE 2051 AA; 229604 MW; D60F8A032F659B00 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.8%; Score 486.5; DB 2
41.1%; Pred. No. 1.4e-37;
iive 45; Mismatches 82
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PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_TP; 2.
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-UTM-2003 (TrEMBLrel. 24, Last ann
RyPTPR2AC protein (Fragment).
                                                                                                                                                                                                                                                                                                                          Pfam; PF00041; fn3; 8.
Pfam; PF00047; ig; 2.
Pfam; PF00102; Y phosphatase; 2.
PRINTS; PR00014; FNTYPBIII.
PRINTS; PR00000; PRTYPHPHTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 41.1%;
Watches 99; Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00060; FN3; B. SMART; SM00408; IGC2; 3. SMART; SM00194; PTPC; 2.
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Q9IBA0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                          Hirudo medicinalis (Medicinal leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
MCBI_TaxID=6421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.0%; Score 488.5; DB 1; Length 1948; 41.9%; Pred. No. 8.6e-38; ive 45; Mismatches 80; Indels 15;
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MEDLINE=98195364; PubMed=9526016;
Gershon T.R., Baker M.W., Nitabach M., Wu P., Macagno E.R.;
             /FTIG-VSP 050021.
Wissing (in isoform PTPS-MEB)
/FTIG-VSP_050022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW; D3D211B18B3866DD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   044328;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Name=HmLAR2;
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Matches 101; Conservative
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REPRESENTATION OF THE PROPERTY

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01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2003 (TrEMBLrel. 24, 18) PTFR2Ab protein (Fragment)
EMBL; AF198450; AAF43607.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 100; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVF-LETFHVTQYFT 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSAGVGRIGVFICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NRDKNRYRDILPYDSTRVPLG-----KNKDYINASYIRIVNHEEEYFYIATQGPLPETIE 56
                                                                Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
"Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
divergence of tissue-specific isoform genes in the early evolution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKFKNRLVNIMPYETTRVCLQPIRGVEGSDYINASFID--GYRQQKAYIATQGPLAETTE
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 15, Last annotation update)
Receptor protein tyrosine phosphatase CRYP-alpha (Fragment).
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
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MEDLINE=20193505; PubMed=10727868;
Johnson K.G., Holt C.E.;
"Expression of CRYP-alpha, LAR, PTP-delta, and PTP-rho in the developing Xenopus visual system.";
Mech. Dev. 92:291-294(2000).
                                                                                                                                                                                                                                                                                            EMBL; AB033886; BAA95193.1; --
GO; GO: 0016787; F: hydrolase activity; IEA.
GO; GO: 0016787; F: hydrolase activity; IEA.
GO; GO: 0004705; F: protein tyrosine phosphatase activity; IEA.
GO; GO: 0006470; P: protein amino acid dephosphorylation; IEA.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR00124; Yyr_PP.
PRINTS; PR00102; Y_phosphatase; 2.
PRINTS; PR0700; PRTYPHPHTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 485.5; DB 2; Length; Pred. No. 2.9e-38; 46; Mismatches 80; Indels
                                                                                                                                                                                                                                                    Ono K.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 468 AA; 53976 MW; 76C975D92D437A86 CRC64;
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PROSITE; PS0038; TYR PHOSPHATASE 1; 2.
PROSITE; PS50006; TYR PHOSPHATASE 2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                          MEDLINE=20219325; PubMed=10754074;
                                                                                                                                                                      Mol. Evol. 50:302-311(2000)
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41.5%;
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Best Local Similarity 41.5'
Matches 100; Conservative
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NCBL_TaxID=8355;
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             487 LREFKVTDARDGOSKIVROFOPTDWPEQGVPKSGEGFIDFIGOVHKTKEQFGQDGPISVH
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Myliobatiformes; Myliobatoidei; Potamotrygonidae; Potamotrygon.
GO; GO:0016797; E:hydrolase activity; IEA.

R GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.

R GO; GO:0004872; F:protein tyrosine phosphatase activity; IEA.

R GO; GO:0004872; F:receptor activity; IEA.

R GO; GO:0006470; F:receptor activity; IEA.

R GO; GO:0006470; F:receptor activity; IEA.

R GO; GO:0006470; F:receptor activity; IEA.

R InterPro; IPR000342; TYR_phosphatase.

R PRINTS; PR00100; PRTYPHPHTASE.

R PROSITE; PS00133; TYR_PHOSPHATASE 1; 2.

R PROSITE; PS00056; TYR_PHOSPHATASE 2; 2.

R PROSITE; PS00056; TYR_PHOSPHATASE 2; 2.
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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
Submitted, (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AB033584; BA495191.1; -.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
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Last annotation update)
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41.5%; Pred. No. 4.1e-38;
tive 46; Mismatches 80
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Mol. Evol. 50:302-311(2000).
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                                                                                                                                                                                                                                                                                                                                       15; Gaps
                                                                                                                                                                                                                                                                                    Query Match 38.7%; Score 484.5; DB 2; Length 468; Best Local Similarity 41.9%; Pred. No. 3.7e-38; Matches 101; Conservative 44; Mismatches 81; Indels 15
InterPro; IPR000387; TVR_phosphatase.
InterPro; IPR000242; Tyr_Pp.
Pfam; PF00102; Y_phosphatase; 2.
RFAINTS; PR00100; Y_phosphatase; 2.
RPAINTS; PR001040; PPTP; 2.
RPOSITE; PS00383; TYR_PHOSPHATASE_1; 2.
RPOSITE; PS50056; TYR_PHOSPHATASE_2; 2.
RPOSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
RPOSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
RPOSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
RPOSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
RPOSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
RPOSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
RPOSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
RPOSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
RPOSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
RPOSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
RPOSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
RPOSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
RPOSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 1, 2004, 12:07:42; Search time 19.7573 Seconds (without alignments) 1134.694 Million cell updates/sec Run on:

1 QNRDKNRYRDILPYDSTRVP......MIQTKEQYQFCYEIVLEVLQ 233 US-09-095-478A-6_COPY_225_457 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	protein-tvrosine-p	ı dı	protein-tyrosine-p	ď	- 1	- 1	receptor tyrosine	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	HPTP beta-like tvr	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	leucocyte common a	leukocyte antigen-
SUMMAKIES	ID	0871	S71625	167630	167629	A54971	A41109	T30938	A41105	138670	I58148	S50893	A56178	150212	S12050	S46217	868700	A48066	S17671	B53978	A53978	\mathbf{z}	B48758	A48758	A38191	D54689	C54689	A57068	A56493	TDHULK
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ø	Query Match	1 6	7.		47.3	ů.	φ.	œ.	œ.	7	7.	7.	۲.	7.	7.	7.	7	ζ.		7	7	7	Ġ	ů	ů	œ.	ů.	ů.	Ġ	ů.
	Score	566	95	92	592.5	84	499	86	9	4	74	4	474.5	471	6		468	9	467.5	9	Ø	'n	461.5	461.5	9	9	46	60.	460.5	60.
	Result No.	н	8	m	41	5	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

leukocyte antigen-	protein-tyrosine-p	protein-tyrosine-p	process cycosine p	brocern-cyrosine-p	protein tyrosine p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p
S46216	A60345	S14294	233899	A33839	I58345	S17669	A57064	860613	S17670	149372	JC2366	568250	A53661	S51005	I38140	JW0049
7	7	Н	٠,	4	N	-	Н	7	ë	~	Н	N	Н	~	7	α
1898	387	363	415	410	1176	1452	1188	1216	1452	405	1189	405	1187	1175	1174	356
36.8	36.7	36.6	3.6.6	0 . 0	36.6	36.6	36.5	36.5	36.5	36.4	36.2	36.2	36.2	36.1	36.0	35.9
	460	459	4 T	60.4	458.5	458	457	457	457	456	454	453	453	452.5	451.5	450
460.5	7															

ALIGNMENTS

44	; 0 s	OM 61 	2I 121 : 2V 280	3V 181 	
RESULT 1 T08716 portein-tyrosine-phosphatase homolog DKFZp566K0524.1 - human (fragment) C;Species: Homo sapiens (man) C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004 C;Accession: T08716 R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, May 1999 A;Reference number: Z16472 A;Accession: T08716 A;Molecule type: mRNA A;Residues: 1-398 cANS> A;Coss-references: UNIPROT:Q9Y406; EMBL:AL050040 A;Experimental source: fetal kidney; clone DKFZp566K0524 C;Genetics: A;Note: DKFZp566K0524.1 F;161-379/Domain: protein-tyrosine-phosphatase homology <ptp></ptp>	Query Match 79.4%; Score 995; DB 2; Length 398; Best Local Similarity 78.0%; Pred. No. 4.3e-85; Matches 181; Conservative 26; Mismatches 25; Indels 0; Gaps	Qy 2 NRDKNRYRDILPYDSTRVPLGKNKDVINASYIRIVNHEEBYPYIATQGPLPETIEDFWQM	Qy 62 VLENNCNVIAMITREIECGVIKCYSYWPISIKEPLEFEHFSVFLETFHYTQYFTVRVFQI 	CY 122 VKKSTGKSQCVKHLQFTKWPDHGTDASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV	QY 182 FICUDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKBQYQFCYEIVLEVLQ 233

RESULT 2 871625

protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 13 - mouse
NyAlternate names: epidermal growth factor-binding protein; serine proteinase
Cybecies: Mus musculus (house mouse)
C;Date: 27-Nov-1997 #sequence revision 12-Dec-1997 #text_change 09-Jul-2004
C;Accession: S71625; S67987; I81210; I81209; S40290
FFChida, D.; Kune, T.; Mukouyama, Y.; Tabata, S.; Nomura, N.; Thomas, M.L.; Watanabe, T.
RyElie: Characterization of a protein tyrosine phosphatase (RIP) expressed at a very ea
A;Title: Characterization of a protein tyrosine phosphatase (RIP) expressed at a very ea
A;Accession: S71625
A;Molecule type: mRNA

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.Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 47.5%;
Matches 111; Conservative 4
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Best Local Similarity 47.6
Matches 111; Conservative
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C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology;
C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain protein; phosphorane-binding domain homology cB41>
F; 566-860/Domain: protein 4.1 membrane-binding domain homology cGLG1>
F; 1089-1165/Domain: GLGF domain homology cGLG1>
F; 1361-1437/Domain: GLGF domain homology cGLG2>
F; 1495-1574/Domain: GLGF domain homology cGLG3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: mRNA, K,,1356-1447,'R,,1449-1454 <RE2>
A,Residues: 1338-1354,'K,,1356-1447,'R,,1449-1454 <RE2>
A,Gross-references: GB:L34561, NID:g806295; PIDN:AAC42055.1; PID:g806296
R,Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
R,Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
A,Bendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
A,Bendriks, W.; Brugman, C.; Zeeuwen, June 1993
A,Bengription: Assessment of the expression levels of murine protein-tyrosine phosphatas A,Reference number: $40280
                                        A;Cross-references: UNIPROT:Q64512; UNIPROT:Q62370; EMBL:D83966; NID:g1232103; PIDN:BAA1
A;Experimental source: strain DBA/2; cell line MEL 745A
                                                                                                                                                   5
                                                                                                                                                receptor-bound
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 QIVKKSTGKSQCVKHLQFTKWPDHGTPASAD---FFIKYVRYVRKSHITGPLLVHCSAGV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL: Z23059; NID: 9438155; PIDN: CAA80594.1; PID: 9438156
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F;2203-2422/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;2274/Active site: Cys (phosphocysteine intermediate) #status predicted
F;2374/Active site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1329-1354, K',1356-1447, R',1449-1454 <RES>
A;Cross-references: GB:L34582; NID:g806297; PIDN:AAC42056.1; PID:g806298
A;Accession: 181209
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                           A;Title: Epidermal growth factor-binding protein activates soluble an A;Title: Epidermal growth factor-binding protein activates soluble an A;Reference number: 867987; MUID:96105375; PMID:7498536
A;Accession: 867987
A;Anolecule type: protein
A;Residues: 1098-1102 < WOL>
A;Experimental source: submaxillary glands
B;Sato, T:;Irie, S.; Kitada, S.; Reed, J.C.
A;Title: FAP-1: a protein tyrosine phosphatase that associates with IA; Title: FAP-1: a protein tyrosine phosphatase that associates with IA; Reference number: 159595; MUID:95232528; PMID:7536343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLGF domain homology <GLG4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                       Wolf, B.B.; Brown, M.D.
BBS Lett. 376, 177-180, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <HEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA A; Residues: 2266-2372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1769-1840/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: I81210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S40290
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change U9-UUI-2004
C;Accession: 167630
R;Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
FEBS Lett. 337, 200-206, 1994
A;Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane
A;Reference number: 153483; MUID:94116679; PMID:8287977
                                                                                                                                                                                                                                                                                                               A; Residues: 1-2294 <RES>
A; Residues: 1-2294 <RES>
A; Residues: 1-2294 <RES>
A; Cross-references: UNIPROT: Q12923; GB: D21211; NID: 9452193; PIDN: BAA04752.1; PID: 9452194
C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology; C; Superfamily: protein tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology; C; Reywords: phosphoric monoester hydrolase
F; 574-868 / Domain: protein 4.1 membrane-binding domain homology <B41>
F; 1182-1258 / Domain: GLGF domain homology <GLG2>
F; 2046-2265 / Domain: protein-tyrosine-phosphatase homology <PTP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Home sapient (man)
C; Species: Home sapient (man)
C; Species: Home sapient (man)
C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C; Accession: 167629
R; MacKawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
R; MacKawa, R.; Imagawa, N.; Nagamatsu, M.; Harada, S.
R; MacKawa, R.; Imagawa, N.; Nagamatsu, M.; Harada, S.
R; MacKawa, R.; Imagawa, N.; Nagamatsu, M.; Harada, S.
R; Reference number: 133483; MUID: 94116679; PMID: 8287977
A; Reference number: 163483; MUID: 94116679; PMID: 9487977
A; Residues: 1-2466 cRES.
A; Residues: 1-2466 cRES.
A; Residues: 1-2466 cRES.
C; Residues: 1-2466 cRES.
C; Reywords: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology; C; Reywords: phosphoric monoester hydrolase
F; 574-868 | Domain: protein 4.1 membrane-binding domain homology cPTP>
F; 2218-2437 | Domain: protein-tyrosine-phosphatase homology cPTP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 2
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Pred. No. 1.3e-46;
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47.6%; Pred. No. 1.4e-46;
tive 41; Mismatches 80;
                                                                                                                                                                                                 A;Accession: 167630
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 3 C;Species: Homo sapiens (man)

human

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A,Accession: A41109
A,Molecule type: MRNA
A,Residues: 1-913 < YAN.
A,Residues: 1-913 < YAN.
A,Cross-references: UNIPROT:P26045; GB:M64572; NID:g179912; PIDN:AAA35647.1; PID:g179913
A,Cross-references: UNIPROT:P26045; GB:M64572; NID:g179912; PIDN:AAA35647.1; PID:g179913
B,Ikuta, S.; Itoh, F.; Hinoda, Y.; Toyota, M.; Makiguchi, Y.; Imai, K.; Yachi, A.
GGstroenterol. 29, 727-732, 1994
A,Title: Expression of cytoskeletal-associated protein tyrosine phosphatase PTPH1 mRNA i
A,Reference number: I55698; MUID:95179278; PMID:7874267
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A;Map position: 9431-9431
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; p. C;Reywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase; 531-308/Domain: protein 4.1 membrane-binding domain homology <B41>
F;516-590/Domain: GLGF domain homology <GLG>
F;670-890/Domain: protein-tyrosine-phosphatase homology <PTP>
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A,Title: Isolation of a cDNA clone encoding a human protein-tyrosine phosphatase with ho
A,Reference number: A41109; MUID:91296738; PMID:1648725
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C;Date: 27-Mar-1992 #sequence_revision 02-May-1994 #text_change 09-Jul-2004
C;Accession: A41109; IS5698
E;Yang, Q; Tonks, N.K.
Proc. Natl. Acad. Sci. U.S.A. 88, 5949-5953, 1991
                                                                                                                                                                                                                         120 QIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRT
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A;Residues: 899-913 <RES>
A;Cross-references: GB:S76309; NID:g913165; PIDN:AAB33583.1; PID:g913166
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                             F;842/Active site: Cys (phosphocysteine intermediate) #status predicted
F;848/Binding site: substrate phosphate (Arg) #status predicted
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39.8%; Score 499; DB 1;
Best Local Similarity 42.0%; Pred. No. 2.2e-38;
Matches 102; Conservative 38; Mismatches 85.
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A)Status: translated from GB/EMBL/DDBJ
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A;Molecule type: mRNA
A;Residues: 1-61,'GS',64-839,'D',841-1210,'I',1212-1383,1389-2299,'QM',2302-2490 <RE2>
A;Cross-references: GB:D21209; NID:G452189; PIDN:BAA04750.1; PID:G452190
C;Genetics:
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A;Gene: GDB:DTPN13
A;Gene: GDB:DTPN13
C;Genetics: GDB:DTPN13
C;Genetics: GDB:DTPN13
C;Genetics: GDB:DTPN13
C;Genetics: GDB:DTPN13
A;Map position: 4Q21.3-4Q21.3
C;Genetics: GDB:DTPN13
C;Genetics: GDB:DTPN13
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C;Genetics: GDB:DTPN13
A;Map position: 4Q21.3-4Q21.3
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C;Genetics: GDB:DTPN13
A;Map position: GGGF domain homology GGG3>
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F;1379-1870/Domain: GLGF domain homology GGG3>
F;1379-1870/Domain: GLGF domain homology GGG3>
F;139-1870/Domain: GLGF domain homology GGG3>
F;189-1987/Domain: GLGF domain homology GGG3>
F;2413/Active site: Cys (phosphocysteine intermediate) #status predicted
F;2413/Active site: Cys (phosphocysteine intermediate) #status predicted
F;2419/Binding site: substrate phosphate (Arq) #status predicted
                                                                                                                                                                                                                                                                                                                                                                      Protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 1 [v N;Alternate names: Fas-associated phosphatase FAP-1; protein-tyrosine-phosphatase hPTP1E (5)Species: Homo sapiens (man) (man) (c)Species: Homo sapiens (man) (man) (c)Species: Homo sapiens (man) (man) (c)Species: Homo sapiens (man) (c)Species: Homo sapiens (man) (c)Species: Homo sapiens (man) (c)Species: Homo sapiens (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (man) (
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A;Molecule type: mRNA
A;Residues: 1-2490 <BAN>
A;Residues: 1-2490 <BAN>
A;Residues: 1-2490 <BAN>
A;Residues: 1-2490 <BAN>
A;Rotes: Sequence shown follows authors' translation at positions 62-63
A;Notes: sequence shown follows authors' translation at positions 62-63
A;Notes: Sequence shown follows authors' translation at positions 62-63
A;Notes: Sequence shown follows authors' translation at protein tyrosine phosphatase with simi A;Reference number: A55114; MUID:95014139; PMID:7929060
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A; Residues: 1-61, 'GS', '64-839,'D', 841-1055,1075-1133,'FH',1136-1210,'I',1212-1383,1389-15
A; Residues: 1-61, 'GS', '64-839,'D', 841-1055,1075-1133,'FH',1136-1210,'I',1212-1383,1389-15
A; Cross-references: GB:X80289; NID:9555030; PIDN:CAA56563.1; PID:9515031
R; Sato, T.; Irie, S.; Kitada, S.; Reed, J.C.
Science 268, 411-415, 1995
A; Title: FAP-1: a protein tyrosine phosphatase that associates with Fas.
A; Reference number: 159595; MUID:95232528; PMID:7536343
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A;Status: translated from GB/EMBL/DDBJ
A;Alele type: mRNA
A;Molecule type: mRNA
A;Residues: 1279-1888 «RES>
A;Cross-references: GB:L34583; NID:g806291; PIDN:AAC41755.1; PID:g806292
A;Cross-references: GB:L34583; NID:g806291; PIDN:AAC41755.1; PID:g806292
B;Molecula N.; Imagawa, N.; Imagawa, N.; Harada, S.
FEBS Lett. 337, 200-206, 1994
A;Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane
A;Reference number: I53483; MUID:94116679; PMID:8287977
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:2419/Binding site: substrate phosphate (Arg) #status predicted
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A,Status: preliminary; translated from GB/EMBL/DDBJ
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protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type J precursor - human N,Alternate names: density enhanced phosphatase-1 (DEP-1); protein-tyrosine phosphatase-c; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 0.1-Mar-1996 #sequence_revision 08-Mar-1996 #text_change 09-Jul-2004
C; Accession: 138670; 152599
R; Ostman, A.; Yang, Q.; Tonks, N.K.
Proc. Natl. Acad. Sci. U.S.A. 91, 9680-9684, 1994
A; Title: Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is enhanced A; Reference number: 138670; MUID:95024024; PMID:7937872
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R; Honda, H; Inazawa, J; Nishida, J; Yazaki, Y.; Hirai, H.
Biood 84, 4186-4194, 1994
A; Title: Molecular cloning, characterization, and chromosomal localization of a novel p
A; Reference number: 152599; MUID: 95086212; PMID: 7994032
A; Accession: 152599
A; Status: preliminary; translated from GB/EWBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residuae: 1-216, LTGVRKAA', 225-26, G', G', 262-285, GTEGGLDASNTERSRA', 302, S', 304, 'TAPVHDJ
A; Cross-references: GB: D37781; NID: 9633072; PIDN: BAA07035.1; PID: 9633073
C; Comment: Enhanced expression of this protein with increasing cell density suggests a
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A;Cross-references: GDB:385040; OMIM:600925
A;Cross-references: GDB:385040; OMIM:600925
A;Cross-references: GDB:385040; OMIM:600925
C;Map position: 19q13.4-19q13.4
C;Function:
A;Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and C;CyComedianily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III repect C;CyComedianily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology since J; fibronectin type III repeat homology si
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A;Residues: 1-1337 <RES>
A;Cross-references: UNIPROT:Q12913; EMBL:U10886; NID:g558754; PID:g558755
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40.8%; Pred. No. ...
40.8%; Mismatches
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R;Gu, M.; York, J.D.; Warshawsky, I.; Majerus, P.W.
R;Gu, M.; York, J.D.; Warshawsky, I.; Majerus, P.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 5867-5871, 1991
A;Title: Identification, cloning, and expression of a cytosolic megakaryocyte protein-ty A;Reference number: A41105; MUID:91288564; PMID:1648233
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C;Species Cert-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30938
R;Gershon, T.R.; Baker, M.; Midpach, M.; Mu, P.; Macagno, E.R.
Submitted to the EMBL Data Library, December 1997
A;Reference number: Z20939
A;Reference number: Z20939
A;Reference number: Z20939
A;Reference number: Z20939
A;Scaus: preliminary; translated from GB/EMBL/DDBJ
A;Kolecule type: mRNA
A;Residues: 1-2051 <GER>
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A;Cross-references: UNIPROT:P29074; GB:M68941; NID:g190747; PIDN:AAA36530.1; PID:g190748
A;Experimental source: megakaryocytes, cell line MEG-10
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C;Date: 20-Mar-1992 #sequence_revision 02-May-1994 #text_change 09-Jul-2004
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                                                                                                                      receptor tyrosine phosphatase - medicinal leech
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protein-tyrosine-phosphatase (EC 3.1.3.48) 2B, splice form LAR - rat
NyAlternate names: leukocyte common antigen-related phosphatase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: IS8148; S46218
R;Walton, K.M.; Martell, K.J.; Kwak, S.P.; Dixon, J.B.; Largent, B.L.
Nehron 11, 38-40, 1993
A;Title: A novel receptor-type protein tyrosine phosphatase is expressed during neurogen
A;Reference number: IS8148; MUID:93357030; PMID:8352946
A;Accession: IS8148
A;Accession: IS8148
A;Accession: LS1848
A;Accession: LS1848
A;Molecule type: mRNA
A;Residues: 1-1501 <ALL>
A;Accession: LS1848
A;Accession: LS1848
A;Accession: LS1848
A;Molecule type: mRNA
A;Residues: 1-1501 <ALL>
A;Coss-references: UNIPROT:064605; GB:L19933; NID:9310242; PIDN:AAA42309.1; PID:9310243
A;Note: in Genbank entry RATYRPHOS, release 113.0, the source is designated as Rattus I R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.
Biochem
J; 302, 39-47, 1994
A;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-pho
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F;47-109/Domain: immunoglobulin homology <IMM2>
F;449-209/Domain: immunoglobulin homology <IMM2>
F;443-506/Domain: immunoglobulin homology <IMM3>
F;482-1506/Domain: immunoglobulin homology <IMM3>
F;882-1501/Domain: pictorectin type III repeat homology <3FR>
F;882-1501/Domain: protein-tyrosine-phosphatase homology <PFP1>
F;1258-1481/Domain: protein-tyrosine-phosphatase homology <PFP2>
F;1481/Domain: protein-tyrosine-phosphatase homology <PFP2>
F;1481/Domain: protein-tyrosine-phosphatase homology <PFP2>
F;1481/Domain: protein-tyrosine-phosphatase homology <PFP2>
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A,Residues: 1-1501 <ZHA>
A,Cross-references: EMBL:L12329; NID:g294573; PIDN:AAC37657.1; PID:g294574
C,Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
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                                                                                                                                                                                                                       RVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKY---VR-YVRKSHITGPLLVHC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 SAGVGRIGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVL 232
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           substrate phosphate (Arg) #status predicted
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41.1%; Pred. No. 7.9e-36;
tive 46; Mismatches 81
                                                                    Score 475; DB 1;
Pred. No. 6.1e-36;
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                                                                    37.9%;
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A,Status: translation not shown
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           F;1245/Binding
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A;Status: preliminary
A;Molecule type: mRNA
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A;Rossidues: 1-1907 <MRG>
A;Cross.references: UNIPROT:Q64494; EMBL:X82288; NID:g587483; PIDN:CAA57732.1; PID:g5874
A;Cross.references: UNIPROT:Qeuwen, P.; Schepens, J.; Wieringa, B.
E;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
A;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
A;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
A;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
A;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
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A;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
A;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
A;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieringa, J.; Wieri
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C;Species: Mus musculus (house mouse)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S50893; 840281
R;Magner, J; Boerboom, D.; Tremblay, M.L.
Bur. J. Biochem. 226, 773-782, 1994
A;Title: Molecular cloning and tissue-specific RNA processing of a murine receptor-type A;Reference number: S50893; MUID:95112841; PMID:7529177
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F;149-209/Domain: immunoglobulin homology <IMM2>
F;449-209/Domain: immunoglobulin homology <IMM2>
F;441-306/Domain: imbronectin type III repeat homology <3FR>
F;128-1907/Domain: fibronectin type III repeat homology <3FR>
F;138-1907/Domain: protein-tyrosine-phosphatase homology <PFP1>
F;154-1887/Domain: protein-tyrosine-phosphatase homology <PFP2>
F;154-1887/Domain: protein-tyrosine-phosphatase homology <PFP2>
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A;Residues: 1441-1501, E/,1503-1546 <HEN>
A;Cross-references: EMBL:223050; NID:9438137; PIDN:CAA80585.1; PID:9438138
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
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41.1%; Pred. No. 1e-35;
:ive 46; Mismatches 8
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Conservative

Indels

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C;Accession: ISO212
R;Stoker, A.W.
Mech. Dev. 46, 201-217, 1994
A;Title: Isoforms of a novel cell adhesion molecule-like protein tyrosine phosphatase an
A;Reference number: ISO212; MUID:95001563; PMID:7918104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:090815; GB:L32780; NID:9485746; PIDN:AAA64460.1; PID:948574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Superfamily: leukocyte antigen-related protein, fibronectin type III repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1314
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                                        7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1372 LÄBFKVTDARDGQSRTVRQFQFTDWPEQGVPKSGEGFIDFIGQVHKTKEQFGQDGPISVH 1431
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DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVF-LETFHVTQYFT 115
                                                                                                                                                                                                                                                               CSAGVGRIGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEV 231
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C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specifi
F;148-298/Domain: immunoglobulin homology <IMM1>
F;245-299/Domain: immunoglobulin homology <IMM2>
F;245-299/Domain: immunoglobulin homology <IRN2>
F;317-399/Domain: leukocyte common antigen cytosolic domain homology <IAC>
F;1157-1479/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1141/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1147/Binding site: Cys (phosphocysteine intermediate) #status predicted
F;1147/Binding site: Cys (phosphocysteine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Č;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSH----ITGPLLVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSAGVGRIGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEV
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41.1%; Pred. No. 1.7e-35;
ive 46; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-tyrosine-phosphatase (EC 3.1.3.48) - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
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A,Gene: CRYPalphal
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rossdues: 390-1912 <KRU>
A;Cross-references: GB:X54133; NID:g35789; PIDN:CAA38068.1; PID:g35790
A;Note: the sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 568-1
A;Note: the sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 568-1
Cancel, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Imai, K.; Yac
Cancel Section -tyrosine phosphatase expression in pre-B cell NALM-6.
A;Reference number: A44929; MUID:92119637; PMID:1370651
                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: A56178; S12052; B44929
R;Pulido, R.; Krueger, N.X.; Serra-Pages, C.; Saito, H.; Streuli, M.
J. Biol. Chem. 270, 6722-6728, 1995
A;Title: Molecular characterization of the human transmembrane protein-tyrosine phosphat
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Rosasides: 1-1912 CPUL>
A; Crosa-references: UNIPROT: P23468; GB:L38929; NID:g755652; PIDN: AAC41749.1; PID:g755653
R; Krueger, N.X.; Streuli, M.; Saito, H.
R; Krueger, N.X.; Streuli, M.; Saito, H.
A; Title: Structural diversity and evolution of human receptor-like protein tyrosine phose
A; Reference number: S12049; MUID:91006018; PMID:2170109
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F;440-209/Domain: immunoglobulin homology <IMM2>
F;440-209/Domain: immunoglobulin homology <IMM3>
F;250-304/Domain: immunoglobulin homology <IMM3>
F;121-811/Domain: immunoglobulin homology <IMM3>
F;711-811/Domain: immunoglobulin homology <IMM3>
F;712-91-1912/Domain: immunoglobulin homology <IMM3>
F;712-91-1912/Domain: protectin type III repeat homology <3FR>
F;1559/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1559/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1850/Binding site: substrate phosphate (Arg) #status predicted
F;1850/Binding site: Substrate phosphate (Arg) #status predicted
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C,Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
                                                                                                                                                                                                                                                                                                                                                                         - human
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          CSAGVGRTGVF1CVDVVFSA1EKNYSFD1MN1VTQMRKQRCGM1QTKEQYQFCYE1VLEV
                                                                                                                                                                                                                                                                                                                                                                      protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor N/Alternate names: protein-tyrosine-phosphatase BPTP-2
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A;Residues: 1756-1804,'C',1806-1845 <ADA>
A;Cross-references: GB:S78086; NID:g243545; PIDN:AAB21147.1; PID:g243546
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A;Note: sequence extracted from NCBI backbone (NCBIN:78086, NCBIP:78087)
A;Note: the authors did not report the entire codon for residue 90
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llarity 41.5%; Pred. No. 1.1e-35;
Conservative 44; Mismatches 82
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Matches 100;
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W.R.; Hashimoto, N.; Ahmad, F.; Ding,
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Best Local Similarity 40.7%
Matches 98, Conservative
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A; Residues: 1872-1911, 'VEMVLQK' < VRI>
A; Accession: 515819
A; Actaus: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1872-1997 < VR2>
A; Relatus: not compared with conceptual translation
A; Relatus: not compared with conceptual translation
A; Relatus: not compared with conceptual translation
A; Relatus: not compared with conceptual translation
A; Relatus: 1872-1997 < VR2>
C; Genetics:
A; Gene: GDB: PTPRB; PTPB
A; Cross references: GDB: 127352; OMIM:176882
A; Map position: 12q15-12q21
C; Superfamily: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III re
C; Reywords: alternative splicing; phosphorotein; phosphoric monoester hydrolase; recept
F; 1-22, 100main: signal sequence # #status predicted < SIT>
F; 23-1697/Domain: extracellular #status predicted < SIT>
F; 125-1642/Domain: intracellular #status predicted < SITA>
F; 1727-1952/Domain: protein-tyrosine-phosphatase homology cPTP>
F; 1727-1952/Domain: protein-tyrosine-phosphatase homology cPTP>
F; 1904/Active site: Cys (phosphocysteine intermediate) #status predicted
F; 1910/Binding site: substrate phosphate (Arg) #status predicted
    protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type beta precursor - human C.Species: Home sapiens (man)
C.Species: Home sapiens (man)
C.Species: Home sapiens (man)
C.Species: Home sapiens (man)
C.Accession: S12050, S15818; S15819
B.Krueger, N.X.; Streuli, M.; Saito, H.
B.Krueger, N.X.; Streuli, M.; Saito, H.
B.Krueger, N.X.; Streuli, M.; Saito, H.
B.Krueger, N.X.; Streuli, M.; Saito, H.
B.Krueger, N.X.; Streuli, M.; Saito, H.
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B.Krueger, N.X.; Streuli, M.; Saito, H.
B.Krueger, N.X.; Streuli, M.; Saito, H.
B.Krueger, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Streuli, M.; Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Title: Expression of a truncated protein-tyrosine phosphatase mRNA in human lung. A,Reference number: S15818; MUID:91243813; PMID:1645282
A,Accession: S15818
A,Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QNRDKNRYRDILPYDSTRVPLGK-----NKDYINASYIRIVNHEEEYFYIATQGPLPETI
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37.5%; Score 469.5; DB 1; Length :
Best Local Similarity 41.2%; Pred. No. 3.2e-35;
Matches 100; Conservative 43; Mismatches 87; Indels
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Bioches, J. 302, 39-47, 1994.

A) Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-ph. A) Areference number: S46216, MUID:94347119; PMID:8068021

A) Accession: S46217

A) Accession: S46217

A) Accession: S46217

A) Accession: S46217

A) Cross-reference nucleic acid sequence not shown

A) Rocecular type: MRNA

A) Residues: 1-1863 CAHA>

A) Cross-references: UNIPROT:064605; EMBL:L11587

R) Goldstein, B.J.

Submitted to the EMBL Data Library, February 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-1788, 'G',1790-1863 (GOL)
A; Residues: 1-1788, 'G',1790-1863 (GOL)
A; Residues: 1-1788, 'G',1790-1863 (GOL)
A; Cross-references: BMS-L11587, NID: 9205134; PIDN: AAC37656.1; PID: 9205135
B; Yan, H.; Grossman, A.; Wang, H.; D'Eustachio, P.; Mossie, K.; Musacchio, J.M.; Silvem J. Biol. Chem. 268, 24880-24886, 1993
A; Fille: A novel receptor tyrosine phosphatase-sigma that is highly expressed in the ne: A; Reference number: A49104; MUID: 94043351; PMID: 8227050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSAGVGRIGVFICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEV
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F;1801/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-596,'R',598-603,'I',967-1788,'G',1790-1863 <YAN>
A;Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: sequence extracted irom web todaced. C;Superfamily: leukocyte antigen-related protein; fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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40.7%; Pred. No. 3.7e-35;
ive 46; Mismatches 82
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December 1, 2004, 12:16:33 ; Search time 424.441 Seconds (without alignments) 195.771 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                         1253
1 QNRDKNRYRDILPYDSTRVP.....MIQTKEQYQFCYEIVLEVLQ 233
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(cgn2_6)ptodata/2/pubpaa/US07 PUBCOMB.pep:*
(cgn2_6)ptodata/2/pubpaa/US07 NEW PUB.pep:*
(cgn2_6)ptodata/2/pubpaa/US06_PUBCOMB.pep:*
(cgn2_6)ptodata/2/pubpaa/US07_NEW PUB.pep:*
(cgn2_6)ptodata/2/pubpaa/US08_PUBCOMB.pep:*
(cgn2_6)ptodata/2/pubpaa/US08_PUBCOMB.pep:*
(cgn2_6)ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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(cgn2_6)ptodata/2/pubpaa/US09_RW PUB.pep:*
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(cgn2_6)ptodata/2/pubpaa/US09_NEW PUB.pep:*
(cgn2_6)ptodata/2/pubpaa/US09_NEW PUB.pep:*
(cgn2_6)ptodata/2/pubpaa/US108_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1582122 seqs, 356623098 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Lind A endemok		· -	, c	٠ آ ر	, 4	, ,	Semience 7 Appli	- 0	, ,	2 1	, p c	sednence IZ, Appl	Sequence 2, Appli
SUMMARIES		ID	US-09-095-478-6	US-09-095-478-8	US-09-095-478-1	US-09-095-478-2	US-09-095-478-3	US-10-311-764-4	US-09-095-478-4	US-09-095-478-7	US-09-095-478-9	US-10-060-065-35	113-10-059-585-56	TIS-10-177-080-12	77-006-111-07-00	US-10-795-148-2
		DB	10	10	10	10	10	15	10	10	10	14	14	4	1	17
		Match Length DB	354	379	426	463	412	420	122	381	358	1267	1267	2466	2 1	2466
,	* Query	Match	100.0	100.0	100.0	100.0	93.7	80.0	53.3	47.8	47.3	47.3	47.3	47.3		47.3
		Score	1253	1253	1253	1253	1174	1003	668	598.5	592.5	592.5	592.5	592.5	1 0	577.5
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Sequence 46, Appl Sequence 46, Appl Sequence 1349, Ap Sequence 5, Appli Sequence 93, Appli	00000	6 2 3 6 7 7 5 6 6 5 5 5 5 6 6 6 6 6 6 6 6 6 6	444 444 444 444 444 444 444 444 444 44	Sequence 44, Appl Sequence 2, Appli Sequence 1670, Ap Sequence 6, Appli Sequence 7, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli
	US-10-218-779- US-10-087-684- US-10-218-779- US-10-072-012- US-09-848-294-2	-293-231-2 -366-547-3 848-294-7 -293-231-7 808-602-55	US-10-366-547-40 US-09-788-626-22 US-09-808-602-54 US-09-800-198-44 US-10-245-539-6 US-10-723-606-3 US-10-390-501-2 US-10-346-547-42	10-366-547-10-366-547-10-408-765A-10-634-027
9 10 10 10	21.51.6	4 6 7 6 1 6 1 6 1 6 1 6 1 6 1 6 1 6 1 6 1	4 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	14 16 15 15 10 10 15
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47.3 47.3 45.2 45.0		8 8 4 4 0 0		
592.5 592.5 592.5 566 566	554 538 538 538 699	4 4 4 4 4 4 4 4 4 4 4 4 4 9 4 9 4 4 9 4 4 9 4 4 9 4 4 9 4 4 9 4 4 9 4 4 9 4 9 4 9	488 483.5 483.5 403.5 475 475	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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ALIGNMENTS

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RESULT 1

US-095-478-6

Sequence 6, Application US/09095478

Sequence 6, Application US/09095478

Publication No. US20030095970A1

SEQUENCE 1 INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

NUMBER OF SEQUENCES:

CORRESPONDENCES:

ADDRESS:

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METHODS
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                                              379 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVE
TITLE OF INVENTION: PHOS
TITLE OF INVENTION: RELA
TITLE OF INVENTION: METH
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acid
                                                                                                   TOPOLOGY: linear ) MOLECULE TYPE: Peptide US-09-095-478-8
                                                                                  single
                                                                  amino acid
                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-095-478-1
TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRVVRKSHITGPLLVHCSAGVGRIG 297
                                                                                                                                                                                                                                                                                                                     MVLENNCNVIAMITREIEGGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQ 120
                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                1 ONRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·.
                                                                                                                                                                                                                                 DB 10; Length 354;
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                               Query Match 100.0%; Score 1253; DB 10; Best Local Similarity 100.0%; Pred. No. 1.4e-125; Matches 233; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gregory
NOVEL PROTEIN TYROSINE
PHOSPHATASE SUPTPO5 AND
RELATED PRODUCTS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/115
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700 STREET: Suite 4700 STREET: California COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INPORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 aming acids
         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOV
TITLE OF INVENTION: PHO
TITLE OF INVENTION: REL
TITLE OF INVENTION: MET
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: LYON & LYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                 single
                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                 TYPE: amino acid STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                       US-09-095-478-6
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61 MVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQ 120
                                                                                                                                                                                                                                                                         121 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTG 180
                                                                                                                 203 MYLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHYTQYFTVRVFQ 262
                                                                                                                                                                                                                                                                                                               263 IVKKSTGKSQCVKHLQFTKMPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTG 322
                                                                                      1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                    181 VFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 233
                                                                                                                                                                                                                                                                                                                                                                                               323 VFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQIKEQYQFCYEIVLEVLQ 375
                                           0;
  Length 379;
                                                Indels
Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-125;
Matches 233; Conservative 0; Mismatches 0; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHATASE SUPTPOS AND RELATED PRODUCTS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plowman, Gregory
VENTION: NOVEL PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/09/095,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 83.1 west Fifth Street
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEX: (67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
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Gaps

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225 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ 284
                                                                                                                                                                                                                                                                                                                                                                                                            61 MVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 WVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQ 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRXVRKSHITGPLLVHCSAGVGRTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               345 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTG 404
                                                                                                                                                                                                                                                                              1 ONRDKONRYRDILPYDSTRVPLGKOKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 VFICVDVVFSAIBKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 233
                                                                                                                                                                                                                     0
                                                                                                                                                 100.0%; Score 1253; DB 10; Length 463; 100.0%; Pred. No. 2e-125; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Plowman, Gregory
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSEHATASE SUPPROS AND
TITLE OF INVENTION: PHOSEHATASE SUPPROS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Sai West Fifth Street
STREET: Suite 4700
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STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: FASTERO FOR Windows 2.0
SOFTWARE: FASTERO FOR Windows 2.0
CURRENT APPLICATION NUMBER: US/09/095,478
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                     Conservative
                                                      MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                    TOPOLOGY: linear
                                                                                                                                              Query Match
Best Local Similarity
Matches 233; Conserv
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                                                                                    US-09-095-478-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 MVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 MVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ 60
                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                            Length 426;
                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                               Query Match
100.0%; Score 1253; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.8e-125;
Matches 233; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPPOS AND
TITLE OF INVENTION: MELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: Store
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REGISTRATION NUMBER: 32,327
REFERNCE/DOCKET NUMBER: 224/115
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
TELEX: 67-3310
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastESC for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
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STREET: 633 West Fifth Street
STREET: Suite 4700
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                    Peptide
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STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                MOLECULE TYPE:
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US-09-095-478-1
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US-09-095-478-2
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                                                                                                                                                                                                                        121 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTG 180
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                                                Gaps
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Length 412;
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APPLICANT: BAUGHW, Mariah R.; DING, Li
APPLICANT: BAUGHW, Mariah R.; DING, Li
APPLICANT: BAUGHW, Mariah R.; DING, Li
APPLICANT: BLIOTT, Vicki S.; GANDHI, Amena R.
APPLICANT: ELLIOTT, Vicki S.; GANDHI, Amena R.
APPLICANT: KERREY, Liam; LEE, Errestine A.
APPLICANT: KERREY, Liam; LEE, Errestine A.
APPLICANT: LU, Yan; NGUYEN, Danniel B.
APPLICANT: REDDY, Roopa M.; RANVIAM, Madhusudan M.; APPLICANT: REDDY, Roopa M.; RANVIAM, Madhusudan M.; APPLICANT: THORNION, Machael B.; TRIBGULEY, Catherine M. APPLICANT: THORNION, Machael B.; TRIBGULEY, Catherine M. APPLICANT: THORNION; PROTEIN PHOSPHATASES
TITLE OF INVENTION PROFEEN PROSPHATASES
TITLE OF INVENTION NUMBER: US/10/311,764
CURRENT FILING DATE: 2001-06-14
PRIOR FILING DATE: 2001-06-14
PRIOR FILING DATE: 2001-06-16
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
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CTHER INFORMATION: Incyte ID No. US20040023245A1 7476861CD1
US-10-311-764-4
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                                                Indels
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80.0%; Score 1003; DB 15;
Best Local Similarity 78.9%; Pred. No. 1.2e-98;
Matches 183; Conservative 24; Mismatches 25;
93.7%; Score 1174; DB 10;
100.0%; Pred. No. 5.2e-117;
iive 0; Mismatches 0;
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Publication No. US20040023245A1
GENERAL INFORMATION:
                                                        218; Conservative
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          Query Match
Best Local Similarity
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LENGTH: 420
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                                                          Matches
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                                                                                                                                                      243 VLENNSNVIAMITREIEGGIIKCYHYWPISLKKPLELKHFRVFLENYQILQYFIIRMFQV 302
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                                                        62 VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI
                                                                                                                                  122 VKKSTGKSQCVKHLQFTKMPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV
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                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: PIOWMAN, Gregory
APPLICANT: PIOWMAN, NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATAGE SUPPOS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
METHODS
METHODS

METHODS
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COMPUTER READBLE FORM:
MEDIUM TYPE: 35" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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SYSTEM: IBM P.C. DOS 5.0
FastSEQ for Windows 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/095,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WATDURY, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                               ; Sequence 4, Application US/09095478
; Publication No. US20030095970A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Lyon & Lyon
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : (213) 489-1600
(213) 955-0440
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity 100.
Matches 122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
OVALUATION OF TITLE OF INVENTION:
RELITILE OF INVENTION:
NELL TITLE OF INVENTION:
NET WELL
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyo
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM COM OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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181 MIWEQKSTVIAMMIQEVEGEKIKCQRYWPNILGKTIMVSNRLRLALVRMQQLKGFVVRAM 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 QIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRT 179
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                           177 GRIGVFICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYBIVLEVL 232
                                                     1 ONRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ
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47.6%; Pred. No. 1e-54;
tive 41; Mismatches 80;
                                                                                                                                                                                                                      Plowman, Gregory
NOVEL PROTEIN TYROSINE
VENTION: PHOSPHATASE SupTPOS AND
VENTION: RELATED PRODUCTS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/095,478
                                                                                                                                                          Sequence 9, Application US/09095478
Publication No. US2030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                 METHODS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 47.6
Matches 111; Conservative
                                                                                                                                                                                                                                    TITLE OF INVENTION: NOY
TITLE OF INVENTION: PHO
TITLE OF INVENTION: REL.
TITLE OF INVENTION: METI
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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                                                                                                                                            US-09-095-478-9
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117 RVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGV 176
                         61 RVFQIVKKSTGKSQCVKHLQFTKWPDHGTFASADFFIKYVRXVRKSHITGPLLVHCSAGV 120
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                                                                                                                                                                                                    Sequence 7, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPTPOS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 470
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: Peptide
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Best Local Similarity
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GR 122
                                                                           GR 178
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                                                                                                                                                                                      US-09-095-478-7
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Matches 118;
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Gaps

301 GTLICIDVVLGLISQDLDFDISDLVRCMRLQRHGMVQTEDQYIFCYQVILYVL 353

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APPLICANT: Chiaki Sence
APPLICANT: Uni-tini Mezu
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-09902
CURRENT APPLICATION NUMBER: US/10/060,065
CURRENT PILING DATE: 2002-01-29
PRIOR PILING DATE: 2002-01-29
PRIOR PLILING DATE: 1999-10-18
PRIOR PILING DATE: 1999-10-18
PRIOR PILING DATE: 1999-10-18
PRIOR PILING DATE: 1999-10-18
PRIOR PELICATION NUMBER: US 60/189,590
PRIOR PILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: UP 11-248036
PRIOR PILING DATE: 1999-07-29
PRIOR FILING DATE: 2000-01-17
PRIOR PELICATION NUMBER: UP 2000-118776
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR PELICATION NUMBER: UP 2000-118776
PRIOR PELICATION NUMBER: UP 2000-118776
PRIOR PELING DATE: 2000-01-11
PRIOR PELING DATE: 2000-05-07
PRIOR PELING DATE: 2000-05-07
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Best Local Similarity 47.5%; Pred. No. 5.4e-54;
Matches 111; Conservative 41; Mismatches 80; Indels 1;
NESULA 1.2 (1000065)
Sequence 35, Application US/10060065)
Publication No. US20030017480A1
GENERAL INFORMATION:
APPLICANT: Toshio Ota
APPLICANT: Takao Isogai
APPLICANT: Tetsuo Nishikawa
                                                                                                                                                                                                                                                                                                                 Kelichi Nagai
Tetsuji Otsuki
Shin-Ichi Funahashi
                                                                                                                                                                                                                                             Shizuko Ishii
Tomoyasu Sugiyama
                                                                                                                                                                                                                           Jun-Ichi Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                           Koji Hayashi
Kaoru Otsuka
                                                                                                                                                                                                                                                                                           Ai Wakamatsu
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LENGTH: 1267
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APPLICANT:
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APPLICANT:
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Gaps

RESULT 11 US-10-055-585-56 Sequence 56, Application US/10059585 ; Publication No. US20030082776A1

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APPLICANT: Franzn, Petra
APPLICANT: Aspenstrm, Pontus
APPLICANT: Hellman, Ulf
APPLICANT: Gonez, Leonel Jorge
APPLICANT: Heldin, Carl-Henrik
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 MVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFTVRVF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 QIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRT 179
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47.6%; Pred. No. 5.4e-54;
tive 41; Mismatches 80; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 GVFICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYBIVLEVL
                                                                                                                                                                       APPLICANT: Makamatau, Astronomy, Applicant: Makamatau, Astronomy, Applicant: Magai, Keiichi
APPLICANT: Nagai, Keiichi
APPLICANT: Ceuki, Tetsuji
APPLICANT: Senco, Chiaki
APPLICANT: Senco, Chiaki
APPLICANT: Senco, Chiaki
APPLICANT: Near, Jun-Ichi
APPLICANT: Near, Jun-Ichi
APPLICANT: Near, Jun-Ichi
APPLICANT: Near, Jun-Ichi
APPLICANT: NEAR, GENES ENCODING PROTEIN
TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
FILER REFERENCE: 06501-09801
CURRENT APPLICATION NUMBER: US/10/059,585
CURRENT APPLICATION NUMBER: US 60/183,322
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR FILING DATE: 1999-10-18
PRIOR PRILNG DATE: 1999-10-18
PRIOR PRILNG DATE: 1000-01-11
PRIOR PRILNG DATE: 1999-01-18
PRIOR PLING DATE: 1999-01-18
PRIOR PLING DATE: 1999-01-18
PRIOR PLING DATE: 1999-07-29
PRIOR PLING DATE: 1999-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/10177980 Publication No. US20030166232A1 GENERAL INFORMATION:
APPLICANT: Saras, Jan
                    Isogai, Takao
Nishikawa, Tetsuo
Hayashi, Koji
Otsuka, Kaoru
Yamamoto, Jun-ichi
Ishii, Shizuko
                                                                                                                                                         Sugiyama, Tomoyasu
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Matches 111; Conservative
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US-10-059-585-56
Ota, Toshio
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US-09-802-669-46
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Best Local Similarity
Matches 111; Conserv
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US-09-802-669-46
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TYPE: PRT
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US-10-619-220-46
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APPLICANT: JERENCIC, JASNA
APPLICANT: LORENEY, GUSTAVO A.
APPLICANT: LORENEY, ROWAN
TITLE OF INVENTION: USE OF BIOMOLECULAR TARGETS IN THE
TITLE OF INVENTION: TREATMENT AND VISUALIZATION OF TUMORS
FILE REFERENCE: ASYT-022
CURRENT APPLICATION NUMBER: US/10/795,148
PRIOR PRILING DATE: 2004-03-04
PRIOR FILING DATE: 2003-03-04
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47.3%; Score 592.5; DB 17; Length
Best Local Similarity 47.6%; Pred. No. 1.3e-53;
Matches 111; Conservative 41; Mismatches 80; Indels
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        CURRENT APPLICATION NUMBER: US/10/177,980
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US/09/080,855
PRIOR FILING DATE: 1998-05-18
PRIOR PLICATION NUMBER: 08/605,583
PRIOR RILING DATE: 1997-02-25
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 47.63
Matches 111; Conservative
FILE REFERENCE: L0461/7030
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Sequence 46, Application US/09802669
| Patent No. US20020004490A1
| GENERAL INFORMATION:
| APPLICANT: Dean, Nicholas M. APPLICANT: Marcusson, Eric G. APPLICANT: Marcusson, Eric G. APPLICANT: Marcusson, Eric G. APPLICANT: Marcusson, Eric G. APPLICANT: Marcusson, Eric G. APPLICANT: Marcusson, Eric G. APPLICANT: Marcusson, Eric G. APPLICANT: Tanay, Hong | TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling | TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling | TITLE OF INVENTION: ANTISER: US/09/802,669 | FRICA PELICATION NUMBER: US 09/665,615 | PRIOR PILLING DATE: 2000-09-18 | PRIOR PILLING DATE: 1999-04-12 | PRIOR APPLICATION NUMBER: US 09/290,640 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR ELING DATE: 1999-04-12 | PRIOR EL
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Sequence 46, Application US/10619220

Publication No. US20040033979A1

SEMERAL INFORMATION:

APPLICANT: Dean, Nicholas M.

APPLICANT: Myart, Jacqueline

APPLICANT: Myart, Jacqueline

APPLICANT: Myart, Jacqueline

APPLICANT: Myart, US/10/619,220

TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling

TITLE OF INVENTION: ANTISENSE: 1SPH-545

CURRENT APPLICATION NUMBER: US/10/619,220

PRIOR FILING DATE: 2003-07-14

PRIOR FILING DATE: 2001-03-01

PRIOR PRIING DATE: 2001-03-01

PRIOR PLIING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: US 09/665,615

PRIOR FILING DATE: 1999-04-12
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; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 46
; LENGTH: 2485
; LENGTH: 2485
; TYPER: PRT
; ORGANISM: Homo sapiens
UGS-10-619-220-46

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/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-566-076-12

US-09-20-640-46

US-09-848-294-2

US-09-848-294-7

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US-09-144-345-37

US-08-446-345-37

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US-08-80-825-21

US-08-80-825-21

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US-08-81-85-2

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1 QNRDKNRYRDILPYDSTRVP.......
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Maximum DB seq length: 200000000
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Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 8, Appli Sequence 9, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli	R NOVEL PROTEIN	
	ALIGNMENTS US/08596291 US/08596291 SONEL JORGE WARL WELSH, LENA WELSH, LENA PRIMARY STRUCTURE AND FUNCTIONAL EXPRESSION OF NUCLEOTIDE SEQUENCES FOR TYROSINE PHOSPHATASES 4 SES SES TYROSINE PHOSPHATASES 1 TYROSINE PLOSPHATASES 4 SERENTELD & SACKS, P.C. TIC AVENUE TYROSINE PROPER TYROSINE TYROS	
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	ALIGNMENTS E TA ("RUCTURE AN I OF NUCLEO HOSPHATASE & SACKS, P E SACKS, P (6,291)	7000
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	0859 CL JO CL JO CHEN MARY RESS OSININ STEP STEP STEP STEP STEP STEP STEP STEP	9 0 "
11 255 11 255 1232 12332 12533 1252 1252 1252 1252	A P-596-291-3 Tuence 3, Application US/08596291 Sent No. 5821075 APPLICANT: GONEZ, LEGNEL JORGE APPLICANT: GONEZ, LEGNEL JORGE APPLICANT: GONEZ, LEGNEL JORGE APPLICANT: GONEZ, LEGNEL JORGE APPLICANT: BARAS, JAN APPLICANT: HELDIN, CARL-HENRIK TITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: EXPRESSION TITLE OF INVENTION: TYPOSINE PH NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: ADDRESSEE: WOLF, GREENFIELD & STREET: 600 ATLANTIC AVENUE CITY: BOSTON TITLE OF DOLOGY CONDITES: IEM PC COMPATIBLE CONDITES: IEM PC COMPATIBLE COMPUTER: PATENTION AND ATA: APPLICATION NUMBER: US/08/596 FILING DATE: 09-AUG-1996 FILING DATE: 01-SEP-1993 PRICANTON NUMBER: US 08/115 PRICAR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICANT AND AND AND AND AND AND AND AND AND AND	ALIONEL/AGEN INFORMATION: NAME: GATES, EDWARD R. REGISTRATION NUMBER: 31,616 REFERENCE/DOCKET NUMBER: 104 TELECOMMUNICATION INFORMATION: TELEFAX: 617/720-3500 TELEFAX: 617/720-2441 TELEFAX: 92-1742 EZEKTEL FORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 2465 amino acids
######################################	291-3 3, Application UG, 3, Application UG, 2MAT: SARAS, JAN CANT: GONEZ, LEONI CANT: GARS, JAN CANT: CLAESSON-WE CANT: HELDIN, CARH COF INVENTION: EXI OF INVENTION: EXI OF INVENTION: EXI OF INVENTION: EXI OF INVENTION: EXI OF INVENTION: EXI OF INVENTION: EXI OF INVENTION: EXI OF INVENTION: EXI OF INVENTION: EXI OF INVENTION: EXI OF INVENTION: EXI OF INVENTION: EXI OF INVENTION: GREE EXI EX BOSTON UT APPLICATION NOTHER: DATE INTO NUMBER: INTO INTO INTO NOTHER: INTO NUMBER: INTO NUM	AGENT LINFO CATION NUMB CELDOCKET NUICATION INNE: 617/720 92-1742 E 1 FOR SEQ I CHARACTERI CHARACTERI
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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	TI 1 Tuence 3, Application US/ SUBERL INFORMATION: APPLICANT: GONEZ, LEONE APPLICANT: GARS, JAN APPLICANT: CLAESSON-WEL APPLICANT: CLAESSON-WEL TITLE OF INVENTION: PRI TITLE OF INVENTION: PRI TITLE OF INVENTION: PRI TITLE OF INVENTION: PRI TITLE OF INVENTION: PRI TITLE OF INVENTION: PRI TITLE OF INVENTION: PRI TITLE OF INVENTION: PRI TITLE OF INVENTION: PRI TITLE OF INVENTION: TRA CORRESPONDENCES: 4 CORRESPONDENCE ADDRESS: A CORPERSEE: WOLF, GREES STREET: BOSTON STRIET: BOSTON STRIET: BOSTON STRIET: BOSTON COMPUTER: BOSTON COMPUTER: END PO COMP COMPUTER: PRIDED OF SOFTWARE: PORM: MEDIUM TYPE: Floppy d COMPUTER: PRIDED OF SOFTWARE: PRIDED OF SOFTWARE: PRIDED OF SOFTWARE: PRIDED OF SOFTWARE: USBELLING DATE: OB-AUG-1 FILLING DATE: USBELL APPLICATION NUMBER: U FILLING DATE: OB-AUG-1 FILLING DATE: OB-AUG-1 FILLING DATE: USBELL APPLICATION NUMBER: U FILLING DATE: OB-AUG-1 FILLING DATE: OB-ER-1	ALLOKABI TAGENI LINFORMATI NAME: GETTES, EDWARD R REGISTRATION NUMBER: REFERENCE/DOCKET NUMBE TELECOMMUNICATION INFORM TELECHONE: 617/720-2441 TELEFAX: 617/720-2441 TELEFAX: 92-1142 EZEKIE INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 2465 amino ac
2 2 2 2 3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5	RESULT 1 US-08-56-291-3 Sequence 3, Application US/08596291 Patent No. 5821075 GENERAL INFORMATION: APPLICANT: GONEZ, LEONEL JORGE APPLICANT: ARAS, JAN APPLICANT: CLAESSON-WELSH, LENA APPLICANT: HELDIN, CARL-HENRIK ITILE OF INVENTION: EXPRESSION ITILE OF INVENTION: EXPRESSION ITILE OF INVENTION: EXPRESSION ITILE OF INVENTION: EXPRESSION ITILE OF INVENTION: EXPRESSION ITILE OF INVENTION: EXPRESSION ITILE OF INVENTION: EXPRESSION ITILE OF INVENTION: EXPRESSION ITILE OF INVENTION: TYROSINE PH NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: ADDRESSEE: WOLF, GREEN'S ATAE: MASSACHUSETTS COUNTRY: BOSTON STREET: GON ATLANTIC AVENUE COMPUTER: IEDR PC COMPATIBLE COMPUTER: IEDR PC COMPATIBLE COMPUTER: IEDR PC COMPATIBLE COMPUTER: IEDR PC COMPATIBLE COMPUTER: PATENTION SYSTEM: PO-DOS/MS-DS SOFTWARE: PATENTION NUMBER: US/08/596 FILING DATE: 09-AUG-1993 PELLING DATE: US-NEWS-TONE	N N TELLIN THE SECTION OF SECTION
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Score 592.5; DB 2; Length 2465; Pred. No. 1.2e-60;

47.38;

Query Match Best Local Similarity

TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein US-08-596-291-3 47.68;

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Best Local Similarity
Matches 111; Conserv
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                                                            APPLICANT: GONEZ, LEONEL JORGE
APPLICANT: SARAS, JAN
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: EXPRASTSON OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
                                                                                                    61 MYLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFTVRVF 119
                                                                                                                                                                 120 QIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYYRKSHITGPLLVHCSAGVGRT 179
                                         1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEBYFYIATQGPLPETIEDFWQ
             Gaps
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             1;
             Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,804
             80;
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              Mismatches
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/596,291
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAMB: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REGISTRATION NUMBER: 10461/7003
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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3R: LO461/7003
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09100804
Patent No. 6066472
                41;
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                  111; Conservative
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US-09-100-804-3
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47.3%; Score 592.5; DB 3; Length 2465;

Query Match

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APPLICANT: STATES, Jan
APPLICANT: Franza, Jan
APPLICANT: Franza, Jan
APPLICANT: Franza, Pontus
APPLICANT: Aspenstrm, Pontus
APPLICANT: Hellman, Ulf
APPLICANT: Gonez, Leonel Jorge
APPLICANT: Heldin, Carl-Henrik
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPLI
TITLE OF INVENTION NUMBER: US/09/080,855A
CURRENT PAPLICATION NUMBER: 08/805,583
EARLIER APPLICATION NUMBER: 08/805,583
EARLIER FILING DATE: 1997-02-25
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FRASESQ for Windows Version 3.0
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47.6%; Pred. No. 1.2e-60;
tive 41; Mismatches 80;
Pred. No. 1.2e-60;
                 41; Mismatches
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Patent No. 6083721
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Best Local Similarity 47.6'
Matches 111; Conservative
                   111; Conservative
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APPLICANT: Saras, Jan
APPLICANT: Franzn, Petra
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US-09-080-855-12
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Patent No. 6204055
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling FILE REPRENEUS: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT PILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
LENGTH: 2485
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                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
                                                                                                                                                                                                                                                                                                                                                                                              47.3%; Score 592.5; DB 5
47.6%; Pred. No. 1.2e-60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              41; Mismatches
                                    TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
TELEX: 92-1142 EZEKIEL.
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2466 amino acids
             TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 47.6%
Matches 111, Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 47.69
Matches 111; Conservative
                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                  amino acid
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US-09-290-640-46
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APPLICANT: Aspenstrm, Pontus
APPLICANT: Hellman, Ulf
APPLICANT: Hellman, Ulf
APPLICANT: Hellman, Ulf
APPLICANT: Heldin, Carl-Henrik
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
CURRENT APPLICANTON NUMBER: US/09/566,076
CURRENT FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2277 MIWEOKSTVIAMMIQEVEGEKIKCORYWPNILGKTTMVSNRLRLALVRMOOLKGFVVRAM 2336
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EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFTVRVF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 QIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ONRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATOGPLPETIEDFWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.3%; Score 592.5; DB 4;
47.6%; Pred. No. 1.2e-60;
rative 41; Mismatches 80;
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APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-5EP-1993
ATTORNEY/AGENT INFORMATION:
NAME: TWOMEY, MICHAEL J.
REGISTRATION NUMBER: P-38,349
REFERENCE/DOCKET NUMBER: LO461/7000WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MASSACHUSETTS
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 01-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application PC/TUS9409943
GENERAL INFORMATION:
APPLICANT:
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STREET: 600 ATLANTIC AVENUE
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APPLICANT:
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TITLE OF INVENTION: FITTLE OF INVENTION: FITTLE OF INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVENTION: INVE
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Best Local Similarity
Matches 111; Conserv
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PCT-US94-09943-2
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39.89
Best Local Similarity 42.09
Matches 102; Conservative
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US-09-848-294-7
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APPLICANT: Tonks, Nicholas K.
TITLE OF INVENTION: Isolation of A CDNA Encoding A No. 6479640e1
TITLE OF INVENTION: Protein Tyrosine Phosphotase Which Localizes to Focal
TITLE OF INVENTION: Adhesions and Uses Therefor
TITLE OF INVENTION: Adhesions and Uses Therefor
FILE REPERENCE: CSHL90-04FZA
CURRENT APPLICATION NUMBER: US/09/848,294
CURRENT APPLICATION NUMBER: 09/235,251
PRIOR PELING DATE: 1999-01-22
PRIOR FILING DATE: 1999-01-22
PRIOR FILING DATE: 1999-01-24
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1990-03-04
PRIOR FILING DATE: 1991-03-01
PRIOR FILING DATE: 1991-03-01
PRIOR FILING DATE: 1991-03-01
PRIOR FILING DATE: 1990-03-14
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2236 ENRRKNRYKNILPYDATRVPLGDEGGYINASFIKIPVGKEEFVYIACQGPLPTTVGDFWQ 2295
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                                                          Parent No. 6653133
; GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Wyatt, Jacqueline
TITLE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0502
CURRENT APPLICATION NUMBER: US/09/665,615B
CURRENT FILING DATE: 2000-09-18
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 179
NUMBER OF SEQ ID NOS: 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                 Sequence 46, Application US/09665615B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-848-294-2
; Sequence 2, Application US/09848294
; Patent No. 6479640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homosapiens
US-09-848-294-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-665-615B-46
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                                US-09-665-615B-46
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PRIOR FILING DATE: 1991-03-01

PRIOR FILING DATE: 1991-03-01

PRIOR PRICATION OF A CDNA Encoding A No. 6479640el

TITLE OF INVENTION: Protein Tyrosine Phosphotase Which Localizes to Focal

TITLE OF INVENTION: Adhesions and Uses Therefor

TITLE OF INVENTION: Adhesions and Uses Therefor

FILE REFERENCE: CSH190-04FZA

CURRENT APPLICATION NUMBER: US/09/848,294

CURRENT APPLICATION NUMBER: 09/235,251

PRIOR APPLICATION NUMBER: 08/759,536

PRIOR PRILING DATE: 1999-01-22

PRIOR PELING DATE: 1995-12-04

PRIOR FILING DATE: 1993-08-16

PRIOR PELING DATE: 1993-08-16

PRIOR PELING DATE: 1991-03-01

PRIOR PILING DATE: 1991-03-01

PRIOR PILING DATE: 1991-03-01

PRIOR PILING DATE: 1991-03-01

PRIOR APPLICATION NUMBER: 07/494,036

PRIOR APPLICATION NUMBER: 07/494,036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 IEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEH--FSVFLETFHVTQ 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 YFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHI-TGPLLVH 171
                                                5
                                                                                                                                                                                                                                                                                                                                           112 QYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHI-TGPLLV 170
                                                                                                                                                                                                                                                                                                                                                                                                                  171 HCSAGVGRIGVFICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLE 230
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                                                                                                                                                                                                         54 TIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEH--FSVFLETFHVT
                                                                                                    1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYI-----RIVNHEBEYFYIATQGPLPE
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39.8%; Score 499; DB 4; Length 913; 42.0%; Pred. No. 3.7e-50;
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Best Local Similarity 41.7%; Pred. No. 2.2e-50;
Matches 101; Conservative 38; Mismatches 85
                                                      38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09848294 Patent No. 6479640
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54 TIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHV--- 110
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                                                                     Sequence 21, Application US/08685992
Patent No. 5912138
GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: TWO Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                    SUFTWARE: FASTSED for Windows 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,992
FILING DATE: 25-UUL-1996
CLASSIFICATION DATA:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.9%; Score 487; DB 2; 41.8%; Pred. No. 1.4e-49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSHL96-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             781-861-9540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 102; Conserva
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TOPOLOGY: lin
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TELEFAX: 7
                                                         JS-08-685-992-21
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173 CSAGIGRTGVLVTMETAMCLTERNLPIYPLDIVRKMRDQRAMMVQTSSQYKFVCEAILRV 232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSAGVGRIGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVL 229
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                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: N.Y.
COUNTRY: U.S.A.
ZID: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,345
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US 08/234,440
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      NOVEL PROTEIN PHOSPHOTYROSINE PHOSPHATASES PTP-D1
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42.0%; Pred. No. 7.8e-50;
tive 37; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                       1155 Avenue of the Americas
                                                                                                                              RESULT 10
US-08-446-345-37
; Sequence 37, Application US/08446345
; Patent No. 5831009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: COTUZZI, LAUTA A.
REGISTRATION NUMBER: 30742
REFRENCE/DOCKET NUMBER: 7683
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEKX: (212) 869-864
TELEX: 66141 PENIE
INFORMATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                                                                   Moller, Niels P.H.
Moller, Karin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 amino acids
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Best Local Similarity 42.05
Matches 100; Conservative
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TITLE OF INVENTION: PHOS
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Ed
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                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Ullrich,
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                                                                       233 YE 234
                                  LQ 233
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APPLICANT:
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Sequence 5, Application US/08348006B
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Matches 100; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK H
                                                                                                                                                                                                                                                      NEW JERSEY
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US-08-800-825A-5
                                                                                                                                                                                                                                                    STATE: NE
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                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                    CITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 TQYFTVRVFQ--IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHI-TGP 167
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38.9%; Score 487; DB 2; Length 242;
Best Local Similarity 41.8%; Pred. No. 1.4e-49;
Matches 102; Conservative 37; Mismatches 79; Indels
                                                                                                                                                                                                                    E: HAMILTON, BROOK, SMITH & REYNOLDS, Two Militia Drive
                                                                                                 APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS,
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSHL96-03Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER: 08/685,992
FILING DATE: July 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-CTELEPHONE: 781-861-6540
TELEPHONE: 781-861-9540
                             US-09-144-925-21; Sequence 21, Application US/09144925; Patent No. 5911979; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS: LENGTH: 242 amino acids
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                                                                                                                                                                                                                                                        CITY:
STATE: MA
COUNTRY: USA
... 02421-4799
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STRANDEDNESS: sir
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US-08-348-006B-5

RESULT 13

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60 OMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVF-LETFHVTQYFTVRV 118
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PATENT NO. 5658756
GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                 ZIP: 07055-0900
COMPUTER REABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC COMPATIBLE
OPERATING SYSTEM:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,006B
FILING DATE:
CLASSIPTCATION: 514
PRIOR APPLICATION NUMBER: US 08/122,032
ATTORNEY/AGENT INFORMATION:
NAMME: HAND, J., MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 186,545
REFERENCE/DOCKET NUMBER: 18992IA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.6%; Score 483.5; DB 1; 42.0%; Pred. No. 7.7e-48;
                                                                                                                                                                                               126 E. LINCOLN AVE., P.O. BOX 2000
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Patent No. 5866397
GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: RUTLEDGE, SU JANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 42.0%; Pred. No. 7.7e-48;
Matches 100; Conservative 44; Mismatches 79; Indels 15;
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Batent No. 6214564

GENERAL INFORMATION:
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: SCHMIDT, AZRIEL
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: 7
CORRESPONDENCE ADDRESSE: J. MARK HAND - MERCK & CO., INC.
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
                     CDNA ENCODING A NOVEL HUMAN PROTEIN TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,825A
FILING DATE: 14-FEB-1997
CLASSIFICATION: 435
TITLE OF INVENTION: TYRUS....
TITLE OF INVENTION: TYRUS...
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: 7
ADDRESSEE: 0. MARK HAND - MERCK & CO., INC.
APPERT: 126 E. LINCOLN AVE., P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18992DA
TELEPHONE, 732-594-3905
TELEPHONE: 732-594-3905
                                                                                                                                                                                                                                                                                        PC-DOS/MS-DOS
                                                                                                                                                                                                ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1911 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
TOPOLOGY: linear
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; MOLECULE TYPE: protein
US-08-800-825A-5
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STATE: NEW JE
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US-09-158-657-5
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1671 KNRLVNIMPYESTRVCLQPIRGVEGSDYINASFID--GYRQQKAYIATQGPLAETTEDFW 1728
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 38.6%; Score 483.5; DB 3; Best Local Similarity 42.0%; Pred. No. 7.7e-48; Matches 100; Conservative 44; Mismatches 79;
                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/800,825
FILING DATE: 14-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J. MARK
REGISTRATION WUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18992DA
TELEPHONE: 732-594-3905
TELEPHONE: 732-594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 732-594-4720
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1911 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1911 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-09-158-657-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
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Search completed: December 1, 2004, 12:18:54 Job time : 25.2076 secs

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1022.379 Million cell updates/sec

QNRDKNRYRDILPYDSTRVP.....MIQTKEQYQFCYBIVLEVLQ 233 US-09-095-478A-6_COPY_225_457 score: Sequence: Perfect

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2002273 seqs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries seq length: 0 seq length: 200000000 Minimum DB Maximum DB

geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:* A Geneseq 23Sep04:* geneseqp1990s.* geneseqp2000s:* geneseqp1980s:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	AAW89249	AAW89250	AAW89251	AAE37994	AAE14454	ABG30845	ADD89795	ADE09123	ADE08106	ABG06042	AAE37996	ADK71863	ABU70688	AAG67637	AAG67458	AAR71498	AAW75999	AAY90272	AAB19343	ADJ69543	ADL27685	ADM53457	AMBGORO	4011700	AD11/203	ADF43232
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AD055173	ADF43234	AAW12522	AAY25156	AAG79333	ADD22982	ADL16189	ADF43230	ADD18742	ADE57117	ADE57121	ADD47019	ADD47015	ADL16191	AAG78282	AAR71726	AAW27225	AAW94027	AAU01459	ADN02662
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39.9	39.8	39.8	39.8	39.8	39.8	39.8	39.8	39.0	39.0	39.0	39.0	39.0	38.9	38.9	38.6	38.6	38.6	38.6	38.5
200	499	499	499	499	499	499	499	488,5	488.5	488.5	488.5	488.5	488	487	483.5	483.5	483.5	483.5	482.5
26	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; lenkaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; AAW89249 standard; protein; 426 AA. entry) 10-MAR-1999 Mouse PTP05 AAW89249; REGULT 1

AAM89249

ID AAW8

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DT 10-M

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W09849317-A2 Mus sp.

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97US-0044428P. 97US-0047222P. 97US-0049477P. 97US-0049756P. 97US-0043914P. 98WO-US008439. 27-APR-1998; 28-APR-1997 20-MAY-1997 11-JUN-1997 11-JUN-1997 23-OCT-1997;

(SUGE-) SUGEN INC.

ů, Markby Onrust S, Peles E, Jallal B, , Hui TH; Courtneidge SA, App H, Clary D, Plowman GD,

WPI; 1999-009434/01. N-PSDB; AAV81744 New nucleic acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.

Claim 2; Page 155-157; 193pp; English.

The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The present sequence represents mouse PTP05. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify

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Sequence 463 AA;
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substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene thereby
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es 233; Conserv
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Jallal B, , Hui TH;

Plowman GD, Clary D, J. Courtneidge SA, App H,

(SUGE-) SUGEN INC.

23-OCT-1997;

18-JUN-1997

WPI; 1999-009434/01. N-PSDB; AAV81745.

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The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The present sequence represents mouse PTP05. The above proteins, other than present sequence represents mouse PTP05. The above proteins, other than CC ALK-7, are protein tyrosine phosphatases (PTP9) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways CC that involve the proteins, particularly cancer (e.g. leukaemia and Lymphoma), while modulators of ALK-7 (which is a type I receptor cy particularly for treating Alzheimer's, Parkinson's or Huntington's cy particularly for treating Alzheimer's, Parkinson's or Huntington's cy diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
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nucleic acid encoding specific protein tyrosine phosphatases - useful identifying specific modulators for treatment and prevention of
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                                                                                                                      Claim 2; Page 157-158; 193pp; English.
                                              for identifying specific modulators t
cancer and neurodegenerative disease.
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that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polymucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene
                                                                                                                                                                                                                                                                                                                                                             The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The present sequence represents mouse PTP05. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways
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Hui TH;
97US-0049914P.
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                                                                                  SUGEN
                18-JUN-1997;
                                        23-OCT-1997;
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MVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQ 120 248 MVLENNCNVIAMITREIECGVIKCXSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQ 307 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTG 180 308 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGFLLVHCSAGVGRTG 367 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ Gaps . 0 93.7%; Score 1174; DB 2; Length 405; Indels VEICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 405 VFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 218 .0 Pred. No. 1e-126; 100.0%; Prea. ... Local Similarity 100. nes 218; Conservative Sequence 405 AA; 121 61 Query Match 181 Best Loca Matches Db à q ð 셤 à g

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Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis; atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer; psoriasis; thromobocytopaenia; developmental disorder; Reiter's syndrome; renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease; neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis; Human kinase and phosphatase (KPP-39) protein. Ą AAE37994 standard; protein; 261 (first entry) 06-NOV-2003 AAE37994; AAE37994

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acquired immune deficiency syndrome; immunosuppressive; Crohn's disease; nootropic; transgenic; dermatitis; multiple sclerosis; diabetes mellitus; allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome; osteoporosis; rheumatoid arthitis; Sjogren's syndrome; ophthalmological; gene therapy; asthma; anticonvulsant; uropathic; pancreatitis
autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome;
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2001US-0343007P.
2001US-0343546P.
2002US-0354388P.
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Marquis JP; Gorvad AE; Griffin JA, Marquis ', Lee S, Hawkins PR; Wilson AD, Swarnakar A, Go ng BM, Ramkunar J, Jin P, ' K, Lehr-Mason PM, Khare R, Sprague WW, Zebarjadian Y, Hafalia AJA, Emerling bu, ... Hafalia AJA, Emerling bu, ... behr-Mason Lehr-Mason Ze Sprague WW, Chien D, Wilsor A, Emerling BM, Harann Baughn MR, Chann en Lee SY, Kable AE,

15-FEB-2002; 2002US-0357675P (INCY-) INCYTE GENOMICS INC.

04-FEB-2002;

WPI; 2003-532894/50. N-PSDB; AAD57366. New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders [e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis, cancer or hepatitis.

Claim 1; Page 242; 282pp; English.

The invention relates to an isolated polypeptide, which is a human kinase and phosphatase (KPP). KPP agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of KPP, particularly cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepatitis, paroxysmal cocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary thromobocytopaenia or cancer), developmental disorders (e.g. renal tubular acidosis, anaemia or mental retardation), neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune, confirmantery disorders (e.g. Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune, allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, allergies, mashiner, shashimoto's thyroiditis, irritable bowel syndrome, cout, Grave's disease, hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis, osteoarthritis, osteoarthritis, osteoarthritis, osteoarthritis, syndrome, uveitis), or viral, syndrome, rheumatoid arthritis, slogren's syndrome, uveitis), or viral, is useful in assessing the effects of exogenous compounds on the capting the property and for creating transpant animals to model human the capting and manner of the capting animals to model human the contact of the contact of the contact of the capting and manner of the contact of the capting and manner of the contact of the contact of the capting and contact of the capting and contact of the capting and contact of the capting and contact of the capting and contact of the capting and contact of the capting and contact of the capting and contact of the capting and contact of the capting and contact of the capting and contact of the capting and contact of the capting and contact of the capting and contact of the capting and contact of the capting and contact of the capting and contact of the capting and contact of the capting and contact The present sequence is human KPP protein disease.

Sequence 261 AA;

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Query Match
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Region Domain

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crespiratory distress syndrome, allergies, amyloidosis, anaemia, attention trespiratory distress syndrome, allergies, amyloidosis, anaemia, atherosclerosis, Crohn's disease, actopic dermatitis, diabetes mellitus, cateborasis, coteoporosis, myocardial or pericardial inflammation, sclerosis, myocardial or pericardial inflammation, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome, cotecoarthritis, Siogren's syndrome, scleroderma, systemic rheumatoid arthritis, Sjogren's syndrome, scleroderma, systemic sclerosis, trauma, neurological disorders include Alzheimer's disease, mental retardation and other developmental disorders of central nervous system such as Down's syndrome, cerebral palsy, periodic paralysis, mental cisorders include activation, disorders such as akathesia, ammesia, catatonia, dyskinesia; developmental disorders include e.g. renal tubular acidosis, Ducheme and effective disorders include e.g. renal tubular acidosis, Ducheme and becker muscular dystrophy, gonadal dysgenesis, hypothyroidism; cell conflictative disorders include e.g. actinic keratosis, arteriosclerosis, atherosclerosis, burstits, cirrhosis, hepatitis, psoriasis and cancer including adenocarcinoma, leukaemia. The polypeptide end polymucleoride cretting an agonist/antagonist, a compound that specifically binds to it cretism and agonist/antagonist, a compound that specifically binds to it crits modulator. The polymucleotide is useful for creating knockin humanised animals (pige) or transgenic animals (mice or rats) to mile human disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 VLENNSNVIAMITREIEGGIIKCYHYWPISLKKPLELKHFRVFLENYQILQYFIIRMFQV 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; tyrosine phosphatase; obesity; diabetes; Parkinson's disease; central nervous system disorder; CNS; cardiovascular disorder; stroke; chronic obstructive pulmonary disease; cancer; multiple sclerosis; Alzheimer's disease; Huntington's disease; congestive heart failure; myocardial infarction; chromosome 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEKSTGTSHSVKQLQFTKWPDHGTPASADSFIKXIRYARKSHLTGPMVVHCSAGIGRTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human disease, for generating a transcript image of a tissue or cell type, which represents the global pattern of gene expression by a particular tissue or cell type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 FICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   severe combined immunodeficiency disease (SCID), adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.0%; Score 1003; DB 5; Length 420; 78.9%; Pred. No. 7e-107; ive 24; Mismatches 25; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human tyrosine phosphatase protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG30845 standard; protein; 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-NOV-2001; 2001WO-EP013794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 420 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG30845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG30845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gandhi AR, Griffin JA;
DB, Patterson C;
EA, Tang YT, Thornton M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and cell
                                      Human; protein phosphatase; PP-4; immune system disorder; AIDS; allergy; neurological disorder; developmental disorder; Alzheimer's disease; cell proliferative disorder; Huntington's disease; arteriosclerosis; renal tubular acidosis; gonadal dysgenesis; cancer; adenocarcinoma; leukaemia; transgenic animal; gene therapy.
       VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Tyrosine specific protein phosphatase active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polypeptide, useful for diagnosing, treating or preventing disorders of growth and development, immune system, neurological proliferation diseases, comprises cancer protein phosphatase
                                                                                                           182 FICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 233
                                                                                                                                          183. .411
/note= "Protein-tyrosine phosphatase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Au-Young J, Baughn MR, Ding L, Elliott VS, Gand
Hafalia A, Kearney L, Lee EA, Lu Y, Nguyen DB,
Ramkumar J, Reddy R, Sanjanwala MS, Stewart EA,
Tribouley CM, Walia NK, Yang J, Yao MG, Yue H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362. .379
/label= Transmembrane domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                       AAE14454 standard; protein; 420 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0212447P.
2000US-0213746P.
2000US-0215210P.
2000US-0216529P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUN-2001; 2001WO-US019442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein phosphatase-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Ty
362. .379
                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-090206/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD24022.
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06-JUL-2000; 2
12-JUL-2000; 2
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22-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
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362

endometriosis; angiogenesis.

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The present invention relates to a new human tyrosine phosphatase

Co polypeptide. The invention is useful for the preparation of a medicament

Co for modulating the activity of human tyrosine phosphatase in a disease

Such as obesity, diabetes, a central nervous system (CNS) disorder.

Chronic obstructive pulmonary disease, cardiovascular disorder or cancer.

The invention is useful for treating a human tyrosine phosphatase

dysfunction related disease, preferably the above mentioned diseases. The

Invention is useful for treating the above mentioned diseases. The

CNS disorder is selected from Parkinson's disease, and the

CR Storder is selected from Parkinson's disease, and the

Cardiovascular disorder is selected from congestive heart failure and

myocardial infaction. The modlecules of the invention are useful in

C diagnostic assays for detecting diseases and abnormalities of the presence of

mutations in the polypundleotide coding the polypeptide of the invention.

C The present amino acid sequence represents the human tyrosine phosphatase

CC

Tyrosine phosphatase gene located on chromosome 10
                                                                                                                                                                                                    New human tyrosine phosphatase polypeptide, the regulation of which is useful for treating obesity, diabetes, cardiovascular or central nervou system disorder, chronic obstructive pulmonary disease and cancer.
                                                                                                                                                                                                                                                                                               Claim 25; Fig 2; 145pp; English.
27-NOV-2000; 2000US-0252912P.
                                                                                                                                      WPI; 2002-575236/61.
                                                                                                                                                         N-PSDB; ABK89178.
                                             (FARB ) BAYER AG
                                                                                           Zhu Z;
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Sequence 398 AA;

161 NREKNRYRDILPYDSTRVPLGKSKDYINASYIRIVNCGEBYFYIATQGPLLSTIDDFWQM 220 62 VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI 121 VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV 181 61 2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQM Gaps FICUDUVESALEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 233 . 79.4%; Score 995; DB 5; Length 398; 78.0%; Pred. No. 5.5e-106; ive 26; Mismatches 25; Indels Matches 181; Conservative Local Similarity Query Match 182 셤 ð g à qq ò

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cancer associated phosphatase; enzyme; human; cancer; tumour; cytostatic;
                                                                                                                                                                                                            immunosuppressive, antidiabetic; neuroprotective; antirheumatic; antiatrintic; antipsoriatic; antiarteriosolerotic; antinflammatory; vulnerary; gynaecological; antiarteriosolerotic; hyperproliferative disease; autoimmune disease; diabetes mellitus; multiple sclerosis; rheumatoid arthritis; psoriasis; atherosclerosis; inflammation; scarring;
                                                                                                                                                       Human DKFZP566K0524 protein SEQ ID NO:10.
                                  ADD89795 standard; protein; 398 AA.
                                                                                                              29-JAN-2004 (first entry)
                                                                         ADD89795;
RESULT 7
ADD89795
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targets for screening pharmaceutical agents that inhibit the growth of tumor cells, or for diagnosing and treating cancer, inflammation or nucleic acids encoding cancer associated phosphatases, useful as 19-MAR-2003; 2003WO-CA000393 28-MAR-2002; 2002US-0368859P (KINE-) KINETEK PHARM INC. WPI; 2003-902934/82. autoimmune disease. N-PSDB; ADD89794 WO2003083102-A2 Homo sapiens Delaney AD;

central nervous

The present invention describes an isolated cancer associated phosphatase nucleic acid. Also described: (1) a method of screening for biologically active agents that modulate a cancer associated phosphatase function; (2) a method for thibiting the growth of a cancer call; (4) methods of screening for targets of a cancer associated phosphatase, where the targets are associated with signal transduction in cancer cells; (5) a compound (C) for the treatment of a pharmaceutical carrier and (C); (7) methods for treating a pharmaceutical carrier and (C); (7) methods for treating a tumour comprising a pharmaceutical carrier and (C); (7) methods for treating a tumour and phosphatase of the present invention has cytostatic, immunosuppressive, determining patient prognosis, or as targets for screening pharmaceutical agents that inhibit the growth or metastasis of tumour cells. The present sequence represents the human cancer associated phosphatase DKFZP566K0524, which is used in the exemplification of the present such as autoimmune disease, diabetes mellitus, multiple sclerosis, rheumatoid arthritis, psoriasis, atherosclerosis, inflammation, scarring, endometriosis or angiogenesis, determining the effectiveness of drugs, antidiabetic, neuroprotective, antirheumatic, antiarthritic, antiarteriosclerotic, antiarthritic, antiarteriosclerotic, antinflammatory, vulnerary, gynaecological and antiangiogenic activities. The cancer associated phosphatases and nucleic acids encoding the proteins are useful for visualising tumours in patients or diagnosing and treating cancer, pancreas, lung, ovarian, liver or colon cancer. The polypeptides and nucleic acids may also be used for treating hyperproliferative diseases, Claim 1; SEQ ID NO 10; 63pp; English.

. 0 VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI 121 280 181 61 221 VLENNSNVIAMITREMEGGIIKCYHYWPISLKKPLELKHFRVFLENYQILQYFIIRMFQV VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV 281 VEKSTGTSHSVKQLQFTKWPDHGTPASADSFIKYIRYARKSHLTGPMVVHCSAGIGRIGV 2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEBYFYIATQGPLPETIEDFWQM Length 398; 79.4%; Score 995; DB 7; Length 39 78.0%; Pred. No. 5.5e-106; ive 26; Mismatches 25; Indels 181; Conservative Query Match Best Local Similarity Sequence 398 AA; 122 62 Best Loca Matches 셤 δ g ð ΩD

340

FICVDVVFSAIBKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCXEIVLEVLQ 233

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FICVDVVFSALEKNYSFDIMNIVTOMRKORCGMIQTKEQYQFCYELVLEVLQ 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 508 AA;
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                                                                                                                                                                                                                                                                                                  WO2003054152-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-APR-2002;
                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                     29-JAN-2004
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Ghosh M,
                                                                                                                                       ADE08106;
          182
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                                                                                                ADE08106
                                                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang J;
Wang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKKSTGKSQCVKHLOFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEKNRYRDILPYDSTRVPLGKSKDYINASYIRIVNCGERFYIATQGPLLSTIDDFWQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEEYFYIATQGPLPETIEDFWQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang
                                                                                                                                                                                      novel gene; novel protein; tissue marker; molecular weight marker;
chromosome marker; genetic disorder; contig.
FLCVDVVFCAIVKDCSFNIMDIVAQMREQRSGMVQTKEQYHFCYDIVLEVLR 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Pest Local Similarity 78.0%; Pred. No. 5.7e-106;
Matches 181; Conservative 26; Mismatches 25; Indels
                                                                                                                                                           Novel protein-related contig polypeptide sequence #189.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W, Ren F, Zhang
Weng G, Zhou P,
Boyle BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 2667; 1177pp; English
                                                                            Ā
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Ghosh M, Xue AJ, Wehrman T, We
Ma Y, Wang D, Chen R, Xu C, B
                                                                            ADE09123 standard; protein; 409
                                                                                                                                                                                                                                                                                                                                                   10-DEC-2001; 2001US-0339739P.
11-DEC-2001; 2001US-0339453P.
14-MAR-2002; 2002US-0365091P.
14-MAR-2002; 2002US-036584P.
12-APR-2002; 2002US-0375381P.
12-APR-2002; 2002US-0375695P.
22-APR-2002; 2002US-001558
                                                                                                                                                                                                                                                                                                                         10-DEC-2002; 2002WO-US039555
                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                    WO2003054152-A2
                                                                                                                                                                                                                                         Unidentified
                                                                                                                                      29-JAN-2004
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         341
                                                                                                            ADE09123;
                                                   RESULT 8
                                                                   ADE09123
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VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed, as molecular weight markers on gels, as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wang J;
Vang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQM
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                                                                                                                                                                                                                                                                                                                                                                          novel gene; novel protein; tissue marker; molecular weight marker;
chromosome marker; genetic disorder.
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                                                                                                                                                                                                                                                                                                                       Novel protein (useful for identifying genetic disorders) #261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang J, Zhao QA,
u P, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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78.0%; Pred. No. 7.8e-106;
iive 26; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YT, Asundi V, Goodrich RW, Ren F, Zhang
n M, Xue AJ, Wehrman T, Weng G, Zhou P,
, Wang D, Chen R, Xu C, Boyle BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; SEQ ID NO 1172; 1177pp; English.
                                                                                                                                                                   Ā
                                                                                                                                                                     ADE08106 standard; protein; 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-DEC-2001; 2001US-0339739P.
11-DEC-2001; 2001US-0339453P.
14-MAR-2002; 2002US-0365091P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 MAR-2002; 2002US-0365384P
12-APR-2002; 2002US-0372381P.
12-APR-2002; 2002US-0372615P.
22-APR-2002; 2002US-00128558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002US-0376045P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-DEC-2002; 2002WO-US039555
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Best Local Similarity 78.0
Matches 181; Conservative
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Pred. No.

78.0%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a cativity of (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving abstrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in disorders for generatic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AbG00010-AbG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in the winy and the printed specification, but was obtained in the winy and the printed specification, but was obtained in the wing and products are applications.
                   VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                          233
                                                                                                                                                                                                                                                                                                                                               Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                       FICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID NO 36401; 103pp; English.
                                                                                                                                                                                                                                                                                                           Novel human diagnostic protein #6033.
                                                                                                                                                                                                    Ā.
                                                                                                                                                                                                ABG06042 standard; protein; 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang
                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                        451
                                                                                                                                                                                                                                    ABG06042;
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Length 561;

DB 4;

Score 995;

79.48;

Query Match

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                                                                                         Gorvad AE;
Griffin JA, Marquis JP;
t, Lee S, Hawkins PR;
                                                                                                                                          VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI 121
                                                                                                                                                                                                               122 VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
                                                                                                                                                                                                                                   444 VEKSTGISHSVKQLQFIKWPDHGTPASADSFIKYIRYARKSHLTGPMVVHCSAGIGRIGV
                                                                     2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQM
                                     Gaps
                                                                                                                                                                                                                                                                                    FICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 233
                                     ..
                                                                                                                                                                                                                                                                                                         Indels
9e-106;
25;
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Hafalia AuA, Emerling BM, Ramkumar J, Jin P,
Baughn MR, Chawla NK, Lehr-Mason PM, Khare R,
Becha SD, Lee SY, Sprague WW, Zebarjadian Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human kinase and phosphatase (KPP-41) protein.
                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 243-244; 282pp; English.
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                                   26;
                                                                                                                                                                                                                                                                                                                                                                                                              AAE37996 standard; protein; 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-DEC-2001; 2001US-0340235P.
19-DEC-2001; 2001US-0343007P.
21-DEC-2001; 2001US-0343546P.
04-FEB-2002; 2002US-0354388P.
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A, Emerling BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer or hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-532894/50
                Best Local Similarity
Matches 181; Conserv
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                                                                                                                                          62
                                                                                                                                                                                                                                                                                    182
                                                                                                                                                                                                                                                                                                                        504
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE37996;
                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                             AAE37996
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26-AUG-2002; 2002US-0406172P. 25-SEP-2002; 2002US-0413910P. 7-SEP-2002; 2002US-0414236P. 11-OCT-2002; 2002US-0417821P.

The invention relates to an isolated polypeptide, which is a human kinase and phosphatase (KPP). KPP agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant cerpression of KPP, particularly cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis, cirhosis, hepatitis, paroxymal cocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary cocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary cocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary cocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary cocturnal haemoglobinuria, polycythaemia vera, psoriasis, primary cocturnal haemoglobinuria retardation), neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune/cocturnal contrological disorders (e.g. Alzheimer) autoimmune thyroiditis, contact dermatitis, contact dermatitis, contact dermatitis, contact dermatitis, contact dermatitis, contact dermatitis, protocoan corposations, pareterial general, in parasitic, protocoan or helminthic infections. The KPP corporation of nucleic acids and kinases and phosphatases. KPP gene is useful in gene therapy and for creating transgenic animals to model human corporation of parasitis sequence is human KPP protein 55555555555555555555555555%&

Sequence 412 AA;

302 VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV 181 62 VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI 121 243 VLENNSNVIAMITREIEGGIIKCYHYWPISLKKPLELKHFRVFLENYQILQYFIIRMFQV 2 NRDKNRYRDILLPYDSTRVPLGKNKDYINASYIRIVNHEBEYFYIATQGPLPETIEDFWQM Gaps .. 75.1%; Score 941; DB 6; Length 412; 78.9%; Pred. No. 1e-99; ative 22; Mismatches 24; Indels FICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKE 219 363 FLCVDVVFCAIVKNCSFNIMDIVAQMREQRSGMVQTKE 400 Query Match
Best Local Similarity 78.9
Matches 172; Conservative 182 122 g 셤 à Op ò 8 δ

ADK71863 standard; protein; 348 AA RESULT 12 ADK71863 PAR SERVICE SE

ADK71863;

20-MAY-2004 (first entry)

Human kinase and phosphatase KPP-40 protein.

human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic; hypotensive; vasotropic; antiinflammatory; antianginal; anti-HIV; antializergic; antiasthmatic; immunosuppressive; antithroid; dermatological; antidabetic; nephrocropic; antigout; gastrointestinal; antirheumatic; antidathritic; uropathic; ophthalmological; antirheumatic; antiparkinsonian; nootropic; anticonvulsant; hepatotropic; antisheumatic; antiparatic; cytostatic; antilpaemic; antiparasitic; antihelmintic; antibacterial; virucide; protozoacide; fundicide; cardiovascular disease; immune system; neurological; growth; development; cell proliferation; viruside; herease; immune system; neurological; growth; development; cell proliferation; viruside; herease; immune system; neurological; growth; development; cell proliferation; viruside; herease; immune system; neurological; growth; development; cell proliferation; viruside; herease; immune system; neurological; growth; development; cell proliferation; viruside; herease; immune system; neurological; growth; development; cell proliferation; viruside; herease; immune system; neurological; growth; development; cell proliferation; viruside; herease; immune system; neurological; growth; development; cell proliferation; viruside; herease; immune system; neurological; growth; development; cell proliferation; viruside; herease; immune system; neurological; growth; development; cell proliferation; viruside; development; cell proliferation; viruside; development; cell proliferation; viruside; development; cell proliferation; viruside; development; cell proliferation; viruside; viruside; viruside; development; cell proliferation; viruside; v helminthic infection; transgenic; gene therapy; enzyme.

Homo sapiens.

25-AUG-2003; 2003WO-US026635.

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The invention relates to a novel isolated polypeptide which is a human kinase and phosphatase (KPP). The polypeptide of the invention demonstrates cardiovascular, antiarteriosclerotic, Mypotensive, vasotropic, antianflammatory, antianginal, anti-HIV, antiallergic, antidiabetic, nephrotropic, antigout, gastrointestinal, neuroprotective, osteopathic, antiarthritic, uropathic, ophthalmological, antiarthritic, uropathic, ophthalmological, antipsoriatic, antiaparkinsonian, nootropic, antionvalsant, hepatotropic, antipsoriatic, antiaparkinsonian, nootropic, antipaemic, antiparasitic, antipsoriatic, antibacterial, virucide, protrozoacide and fungicide activities. The mithacterial, virucide, protrozoacide and fungicide activities. The kinase and phosphatase (KPP) polymucleotides, polypeptides, agonists and antagonists may be useful for diagnosing, treating or preventing contrological disorders and viral, hacterial, fungal, parasitic, proliferative disorders and viral, bacterial, fungal, parasitic, proliferative disorders and viral, bacterial, fungal, parasitic, invention may be useful for creating transgenic animals to model human disease and during gene therapy, the current sequence is that of a human control of the invention.
                                                                                                                                                                 , Richardson TW, Marquis JP, Swarnakar A, Tang YT;
Emerling BM, Jin P, Wilson AD, Yue H, Gietzen KJ;
Yang YG, Lee SY, Khare R, Elliott VS, Hafalia AJA;
, Ramkumar J, Gururajan R, Tribouley CM, Chien D, Tran UK;
                                                                                                                                                                                                                                                                                                                                                                New human kinases and phosphatases, useful for diagnosing, treating or preventing atherosclerosis, hypertension, AIDS, allergy, multiple sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 40; 347pp; English.
                                                                                                                                                                                                                                                                                                         WPI; 2004-226830/21.
N-PSDB; ADK71922.
                                                                                                                            (INCY-) INCYTE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                            or hepatitis.
                                                                                                                                                                            Baughn MR,
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Murage J;
                                                                                                                                                                                                                          Chang H,
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Sequence 348 AA;

ij, 302 122 VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV 181 305 183 NREKNRYRDILPYDSTRVPLGKSKDYINASYIRIVNCGEEYFYIATGGFLSTIDDFWQM VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI 243 VLENNSNVIAMITREIEGGIIKCYHYWPISLKKPLELKHFRVFLENYQILQYFIIRMFOV 2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEBEYFYIATQGPLPETIEDFWQM 51.0%; Score 639; DB 8; Length 348; 54.3%; Pred. No. 7.9e-65; ive 18; Mismatches 16; Indels 72; Gaps Matches 126; Conservative Query Match Best Local Similarity VEK----62 303 g g ð 셤 δ

182 FICVDVVFSALEKNYSFDIMNIVTOMRKORCGMIQTKEQYQFCYEIVLEVLQ 233 ABU70688 standard; protein; 766 AA 306 RESULT 13 ABU70688 ò

ABU70688;

Wed Dec

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The invention relates to a complex between two interacting proteins in adipocyte cells, given in the specification. The proteins are identified by selecting a bait protein from a known adipocyte marker and then complex betroforming a bait protein selection to isolate prey proteins encoded by performing a yeast 2-hybrid selection to isolate prey proteins encoded by members of an adipocyte cDNA library. The proteins are designated SID (RTM) (selected interacting domains) proteins. Also included are a combinant host cell expressing at least one of the interacting recombinant host cell expressing at least one of the interacting collypeptides of the complex, selecting a modulating compound in adipocyte cells, a SID (RTM) polypeptide comprising any of the 738 amino acid sequences given in the specification (including its fragment or variant), a sequence siven in the specification (including its fragment or variant), a vector comprising the Vector, a protein chip comprising the polypeptides and a recombinant host cell for comprising the vector, a protein chip comprising the polypeptides, polypucleotides and compounds are useful for record comprising the vector, a protein chip comprising the polypucleotides and compounds are useful for The polypucleotides and compounds are useful for gartening or treating metabolic disorders such as obesity or diabetes. The polypucleotides are useful as probes or primers. The complex is particularly useful for identifying selected interaction, thus (RTM) for screening drugs that modulate the protein interaction, thus complex in the invantion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as obesity or diabetes.
                                                                                        Human; prey; adipocyte, SID; selected interacting domain; anorectic; antidiabetic; protein-protein interaction; diabetes; yeast 2-hybrid assay; metabolic disorder; obesity.
                                            Human adipocyte Selected Interacting domain, SID, #319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 208-209; 382pp; English.
                                                                                                                                                                                                                                                                                                                                                              14-MAR-2001; 2001US-0275734P.
                                                                                                                                                                                                                                                                                                                    14-MAR-2002; 2002WO-EP003768
    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Daviet L;
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                                                                                                                                                                                                                                                                                                                                                                                                           (HYBR-) HYBRIGENICS
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                                                                                                                                                                                                                           WO200286122-A2.
                                                                                                                                                                                 Homo sapiens.
    10-JUN-2003
                                                                                                                                                                                                                                                                        31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Legrain P,
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576
                                                                                                    MVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFTVRVF 119
                                                                                                                                      636
                                                                                                                                                                179
                                                                                                                                                                          9
                                                  QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ
                                                                    577 MIWEOKSTVIAMMIQEVEGEKIKCQRYWPNILGKIIMVSNRIRLALVRMQQLKGFVVRAM
                                                                                                                                                        QIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRT
                               Gaps
                               1,
 47.3%; Score 592.5; DB 6; Length 766; 47.6%; Pred. No. 6e-59;
                             Indels
        .5,
6e-59,
80,
                            Mismatches
                           41;
                         Conservative
            Local Similarity
                           111;
                                                                            517
                                                                                                                                                         120
                                                                                                      61
Query Match
              Best Loca
Matches
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1078 MIWBOKSTVÍAMMÍQEVEGEKÍKCORÝWPNILGKTTMVSNRLRLALVRMQQLKGFVVRAM 1137

Dp

120 QIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRT 179

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1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The specification describes human protein kinase/protein phosphatases. It is expected that the protein kinase/protein phosphatase gene participates in signal transduction in cells. The protein kinase/protein phosphatase polypeptides and polynucleotides are useful for developing diagnostics and treatment agents for human and animal diseases. The protein kinase/protein phosphatase polypeptides are useful as target molecules in designing novel drugs. The protein kinase/protein phosphatase polyputuleotides are useful as a source of probes and primers, which may be used to isolate homologous sequences. The present sequence represents a human protein, which is used in the course of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1018 ENRRKNRYKNILDPYDATRVPLGDEGGYINASFIKIPVGKEEFVYIACQGPLPTTVGDFWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saito K, Yamamoto J_i, Otsuki T, Funahashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New genes encoding proteins with protein kinase/protein phosphatase activity, useful in the diagnosis and treatment of diseases.
                  Human; protein kinase; protein phosphatase; signal transduction.
180 GVFICVDVVFSAIEKNYSFDIMNIVTOMRKORCGMIQTKEQYQFCYEIVLEVL
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47.6%; Pred. No. 1.2e-58;
iive 41; Mismatches 80;
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T, Wakamatsu A, Nagai K,
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                                                                                                                                                                                          Amino acid sequence of a human protein.
                                                                                                     AAG67637 standard; protein; 1267 AA
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99US-0159590P.
2000JP-00118776.
2000US-0183322P.
2000JP-00183767.
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Sugiyama T,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1267 AA;
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17-FEB-2000;
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Senoo C,
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1138 TLEDIQTREVRHISHLNFTAWPDHDTPSQPDDLLTFISYMRHIHRSGPIITHCSAGIGRS 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Sugiy<sub>g</sub>ma T, Wakamatsu A, Nagai K, Otsuki T, Funahashi S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New genes encoding protein kinase and protein phosphatase, useful for identifying modulators which can be used to treat human or animal disorders associated with the expression or function of these enzymes.
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                                               GVFICUDVVFSALEKNYSFDIMNIVTOMRKORCGMIQIKEOYQFCYEIVLEVL 232
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                                                                                                                                                                                                                                                                   Human; protein kinase; protein phosphatase; signal transduction; intracellular signalling pathway.
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                                                                                                                                                                                                                                         of a human polypeptide.
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                                                                                                                                                  AAG67458 standard; protein; 1267 AA
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18-OCT-1999; 99US-0159590P.
11-JAN-2000; 2000JP-00118776.
17-FEB-2000; 2000US-0183322P.
02-MAY-2000; 2000UP-00183767.
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Ishii S,
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120 QIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRT 179

1 ONRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2004
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OM protein - protein search, using sw model

1, 2004, 12:07:39 ; Search time 85.8421 Seconds
 (without alignments)
1561.731 Million cell updates/sec December on:

US-09-095-478A-5_COPY_188_420

1 QNRDKNRYRDILPYDSTRVP......MIQTKEQYQFCYEIVLEVLQ 233 **BLOSUM62** Scoring table: Sequence:

1253

Perfect score:

1825181 seqs, 575374646 residues Searched:

Gapop 10.0 , Gapext 0.5

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: uniprot_sprot:* 2: uniprot_trembl:* UniProt 02:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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SEQUENCE FROM N.A.
STRANN=C5/BL/6J; TISSUE=Testis;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                     01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Protein-tyrosine-phosphatase (EC 3.1.3.48) (Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4921505B14 product:protein tyrosine phosphatase, non-receptor type 20, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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MEDLINE=98070510; PubMed=9407093;
MEDLINE=98070510; NubMed=9407093;
Obsugi M., Kuramochi S., Matsuda S., Yamamoto T.;
"Molecular cloning and characterization of a novel cytoplasmic protein-tyrosine phosphatase that is specifically expressed in spermatocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=927923; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                   426 AA.
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SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Testis;
MEDLINE-210856G; PubMed=11217851;
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STRAIN=C57BL/6J, TISSUE=Testis;
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RA Adachi J. Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Alzawa K., Akimura T., Hara A., Hashizume W., Ayashida K., Hayateu N., Hiramoto K., Hiracka T., Hirozane T., RA Hayshida K., Hayateu N., Hiramoto K., Hiracka T., Hirozane T., RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kanaka J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Rowal M., Koya S., RA Katoh H., Sawai J., Miyazaki A., Murata M., Nakamura M., Ra Saito R., Saitoh H., Sakai C., Sakai K., Ohno M., Ohsato N., Okazaki Y., A Saito R., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., A Tagawa A., Takahashi F., Takahu-Akahira S., Takeda Y., Tanaka T., A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Buni L., Subnitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MYLENNCHVIAMITREIECGYIKCYSYMPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQ 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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      prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                STRAIN=CSTBL/GJ; TISSUB=Testis;

MEDLINE=20530913; PubMed=11076661;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Kitsunai T., Tashiro H., Itoh M., Nombo H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Harada A., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Ookazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Rawai J., Rake innegrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D64141; BAA23611.1; --. LIE ENIDAL, CELEBALIN, DELGALIN, DELGALIN, DATA AKO29493; BAC26476.1; --. R EMBL; AKO29493; BAC26476.1; --. R EMBL; AKO29493; BAC26476.1; --. R EMBL; AKO29493; BAC26476.1; --. R EMBL; AKO29493; BAC26476.1; --. R EMBL; AKO29493; BAC26476.1; --. R GO; GO:0016787; F:Proceptor octivity; IEA. GO; GO:0004872; F:Proceptor activity; IEA. GO; GO:0004872; F:Proceptor activity; IEA. GO; GO:0004870; P:Proceptor activity; IEA. GO; GO:0006470; P:Proceptor activity; IEA. R InterPro; IPR000387; TYR_phosphatase.

R InterPro; IPR001024; Tyr_PP.
R PRINTS; PR00100; PRITYPHPHTASE.
R SWART; SM00194; PTPC; 1.
R PROSITE; PS00056; TYR_PHOSPHATASE_1; 1.
R PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          426 AA; 49118 MW; 2B35FB13379502F4 CRC64;
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RESULT 2 09Y406

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62 VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                    A Ameorge W. Wirkner U., Mewes H.W., Gassenhuber J., Wiemann S.; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AL050040; CAB43248.1; -. EMBL, AL050040; CAB43248.1; -. EMBL; AL050040; CAB43248.1; -. EMBL; AL050040; CB9716; TOB716.

R GO; GO:0016787; F:hydrolase activity; IEA.

R GO; GO:0006470; P:protein tyrosine phosphatase activity; IEA.

R GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

R InterPro; IPR000242; TYR phosphatase.

R InterPro; IPR00102; Y_PRPC; TyR PP.

R PERM: RROUGO; PRPC; TyR PP.

R PRIM: RROUGO; PRPC; TyR PP.

R PRIM: SMART; SM00194; PTPC; 1.
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S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECTEBRICE FROM N.A.
Vega Q.C., Walton K.M., Dixon J.E.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 5 PDZ/DHR domains.
EMBL; UZ0807; AAA73516.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398 AA; 45690 MW; 857AAD03747870A2 CRC64;
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Last annotation update)
                 Last sequence update)
                                                         Hypothetical protein DKFZp566K0524 (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
Hydrolase; Hypothetical protein.
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Created)
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2004 (TrEMBLrel. 26,
(TrEMBLrel. 12, (TrEMBLrel. 12, 1 (TremBLrel. 24, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 78.0 Matches 181; Conservative
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                                                                                                            Homo sapiens (Human).
                                                                                      Name=DKFZp566K0524;
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                        NCBI_TaxID=9606;
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220

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EMBL;
EMBL;
      2235 BNRRKNYKYKNILPYDATRVPLGDEGGYINASFIKIPVGREBFVYIACQGPLPTTVGDFWQ 2294
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Q64512; Q61494; Q62135; Q64499;
29-MAR-2004 (Rel. 43, Lax sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Protein tyrosine phosphatase, non-receptor type 13 (EC 3.1.3.48)
(Protein tyrosine phosphatase PTP-BL) (Protein-tyrosine phosphatase NTP-BL) (Protein tyrosine phosphatase PTP-BL) (Protein tyrosine phosphatase PTP-BL) (Mouse)
Name=Ptpn13; Synonyms=Ptp14;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 GVFICVDVVFSALEKNYSFDIMNIVTOMRKORCGMIQTKEQYQFCYEIVLEVL 232
        R GO; GO: 000512; C::cytoskeleton; IEA.
R GO; GO: 000515; F::pydrolase activity; IEA.
R GO; GO: 0005515; F::protein binding; IEA.
GO; GO: 0006515; F::protein binding; IEA.
GO; GO: 000470; F::protein tyrosine phosphatase activity; IEA.
GO; GO: 0006470; P::protein tyrosine phosphatase activity; IEA.
GO; GO: 0006470; P::protein amino acid dephosphorylation; IEA.
R InterPro; IPR003059; RERM
R InterPro; IPR001009; Kinase like.
R InterPro; IPR001009; Kinase like.
R InterPro; IPR001478; PDZ.
R InterPro; IPR001478; PDZ.
R InterPro; IPR001478; PDZ.
R InterPro; IPR000387; TYR phosphatase.
R Pfam; PF00373; Band 41; T.
R Pfam; PF00373; Band 41; T.
R Pfam; PF00595; PDZ. 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                           Length 2484;
                                                                                                                                                                                                                                                                                                                                                                                                                                 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                  276382 MW; 45A92F0D4F1ED13D CRC64;
                                                                                                                                                                                                                             SWART; SW00295; B41; 1.

SWART; SW00750; KIND; 1.

SWART; SW00750; KIND; 1.

SWOOTS, PDC, 5.

SWOOTS, PSOOGO; PERM, 1; FALSE NEG.

PROSITE; PSOOGO; PERM, 1; FALSE NEG.

PROSITE; PSOOGO; PERM, 3; 1.

PROSITE; PSOOGO; PERM, 3; 1.

PROSITE; PSOOGO; PERM, 3; 1.

PROSITE; PSOOGO; PERM, 3; 1.

PROSITE; PSOOGOS; TYR_PHOSPHATASE_1; FALSE_NEG.

PROSITE; PSOOGOS; TYR_PHOSPHATASE_2; 1.

PROSITE; PSOOGOS; TYR_PHOSPHATASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                        48.5%; Score 607.5; DB 2;
48.9%; Pred. No. 3.5e-49;
live 40; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
STRAUNECSPEL/6; TISSUB=Skin;
MEDLINE=96340953; PubMed=8749712;
                                                                                                                                                                                            Pfam; PF0102; Y phosphatase; 1. PRINTS; PR00935; BAND41. PRINTS; PR00700; PRTYPHPHTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 48.99
Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 2484 AA;
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                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                         at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98155214; PubMed=9487134;
Cuppen E., Gerrits H., Pepers B., Wieringa B., Hendriks W.;
"PDZ motifs in PTP-BL and RIL bind to internal protein segments in the
Hendriks W., Schepens J., Baechner D., Rijss J., Zeeuwen P., Zechner U., Hameister H., Wieringa B.; "Molecular cloning of a mouse epithelial protein-tyrosine phosphatase with similarities to submembranous proteins."; Cell. Biochem. 59:418-430(1995).
                                                                                                                                                                                                STEAIN=DBA/2;
MEDLINE=95145716; PubMed=7843407;
Chida D., Kume T., Mukouyama Y., Tabata S., Nomura N., Thomas M.,
Chida D., Kume T., Oishi M.;
"Characterization of a protein tyrosine phosphatase (RIP) expressed
a very early stage of differentiation in both mouse erythroleukemia
and embryonal carcinoma cells.";
FEBS Lett. 358:233-239 [1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Biol. Cell 9:671-683(1998).
-!- FUNCTION: Regulates negatively PAS-induced apoptosis and NGFR-mediated pro-apoptoric signaling.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hendriks W., Schepens J., Brugman C., Zeeuwen P., Wieringa B., A. novel receptor-type protein tyrosine phosphatase with a single catalytic domain is specifically expressed in mouse brain."; Biochem. J. 305:499-504(1995).
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STRAIN=CB.17 SCID; TISSUE=Thymus;
MEDLINE=94354845; PubMed=8074693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BALB/c; TISSUE=Brain;
MEDLINE=95134232; PubMed=7832766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 2267-2373 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERACTION WITH PDLIM4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIM domain protein RIL.
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PIR; PT0635; PT0696.
PIR; PT0649; PT0712.
PIR; S40290; S40290.
PIR; S71625; S71625.
                                                                                                                                                                              SEQUENCE FROM N.A.
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PIR; (
PIR; (
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2317 MVWEQNSSVISMMTQEIEGGKIKCORYWPEEPGRPLMIS--NOLQLTLVMTQHLESFVLR 2374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2435 RSGTLICIDVMLALISKOLEFDISNWVHTWRLQRHGNIQTEEQXIFCYQVILYILK 2490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
01-0CT-2004 (Rel. 45, Last annotation update)
Protein tyrosine phosphatase, non-receptor type 13 (EC 3.1.3.48)
(Protein-tyrosine phosphatase IE) (PTP-EI) (hPTPEI) (PTP-BAS)
(Protein-tyrosine phosphatase PTPLI) (Ras-associated protein-tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 MYLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQY---FTVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 RIGVFICUDVVFSALEKNYSFDIMNIVTOMRKORCGMIQTKEGYOFCYEIVLEVLQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94350988; bubMed-8071359; Ben S.-H.; Benville D., Ahmad S., Stocco R., Shen S.-H.; Banville D., Ahmad S., Stocco R., Shen S.-H.; a novel protein-tyrosine phosphatase with homology to both the cytoskaletal proteins of the band 4.1 family and junction-associated guanylate kinases."; J. Biol. Chem. 269:22320-22327 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               дагаты STANDARD; PRT; 2485 AA.
Q12923; Q15159; Q15264; Q15265; Q16674; Q16826; Q8IWH7;
Q9NYN9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

47.5%; Score 595.5; DB 2; Length 2500;
Best Local Similarity 47.0%; Pred. No. 5.2e-48;
Matches 111; Conservative 48; Mismatches 72; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Lisovsky M.Y., Itoh K., Sokol S.Y.;
Lisovsky M.Y., Itoh K., Sokol S.Y.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY327257, ARR97566.1; -.
NON TER 2500
SEQUENCE 2500 AA; 277694 MW; DODD27366EA19CA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277694 MW; D0DD27366EA19CA0 CRC64;
                                                                                                                                                                01-0CT-2004 (TrEMBLrel. 28, Created)
01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Prizzled-8 associated multidomain protein (Fragment)
                                                                                                                          PRT; 2500 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphatase 1) (FAP-1).
Name=PTPN13; Synonyms=PTP1E, PTPL1, PNP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 4).
TISSUE=Breast carcinoma;
                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                          Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 QIVKKSTGKSQCVKHLQFTKWPPHGTPASAD---FFIKYVRYVRKSHITGPLLVHCSAGV
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HIRNSNCAPSFSN -> TSGTASRAFVSY (in Ref
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                                                                                                                                                                                                                    RRINTS; EN00100; FALL.

RAMART; SM00295; B41; 1.

SMART; SM00295; B41; 1.

DR SMART; SM00194; PTDC; 1.

DR SMART; SM00194; PTDC; 1.

DR SMART; SM00194; PTDC; 1.

DR PROSITE; PS00660; FERM. 1; FALSE_NEG.

DR PROSITE; PS00061; FERM. 2; FALSE_NEG.

DR PROSITE; PS00066; PERM. 3; PALSE_NEG.

DR PROSITE; PS00065; TYR PHOSPHATASE_1; FALSE_NEG.

DR PROSITE; PS00093; TYR PHOSPHATASE_2; 1.

DR PROSITE; PS00055; TYR PHOSPHATASE_2; 1.

DR PROSITE; PS00055; TYR PHOSPHATASE_2; 1.

PROSITE; PS00055; TYR PHOSPHATASE_2; 1.

PROSITE; PS00055; TYR PHOSPHATASE_2; 1.

DR PROSITE; PS00056; TYR PHOSPHATASE_1; FALSE_NEG.

PROSITE; PS00056; TYR PHOSPHATASE_2; 1.

PROSITE; PS00056; TYR PHOSPHATASE_2; 1.

PROSITE; PS00056; TYR PHOSPHATASE_2; 1.

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K -> E (in Ref. 2).

S -> L (in Ref. 2).

S -> T (in Ref. 2).

S -> T (in Ref. 3).

QTPHVXXYSFVTEDNT ->
Ref. 1).

D -> H (in Ref. 1).

D -> H (in Ref. 1).

N -> I (in Ref. 2).

S -> P (in Ref. 1).

N -> I (in Ref. 2).

S -> N (in Ref. 2).

D -> N (in Ref. 2).

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Poly-Leu.
                        PDB; 10ZI; NWR; A=1351-1444.

MGD; MGI:103293; Ptpn13.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000299; Band 4.1.
InterPro; IPR000397; PDZ.
InterPro; IPR000387; TYR_Phosphatase.
InterPro; IPR000342; TYr_PP.
Pfam; PF00373; Band 41; 1.
Pfam; PF00102; Y_PPOPIATS; PR01025; Zyhophatase; 1.
PRINTS; PR00102; Zyhosphatase; 1.
PRINTS; PR00102; RAND41.
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PubMed=14516276; DOI=10.1042/BJ20031154;

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EMBL;
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EMBL;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
M. Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A. Klausner R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.,
M. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,
M. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong I.,
M. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong I.,
M. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong I.,
M. Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
M. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Mare M.J., Gay L.J., Hulyk S.W.,
M. Rochards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
M. Helton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Sakalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Sakalska U., Smailus D.E.,
M. Gennien And initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                        Saras J., Claesson-Welsh L., Heldin C.-H., Gonez L.J.; "Cloning and Characterization of PTPL1, a protein tyrosine phosphatase with similarities to cytoskeletal-associated proteins."; J. Biol. Chem. 269:24082-24089[1994]
                                               MEDLINE=94116679; PubMed=8287977;
Maekawa K., Imagawa N., Nagamatsu M., Harada S.;
"Molecular cloning of a novel protein-tyrosine phosphatase containing
a membrane-binding domain and GLGF repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERACTION WITH TRIP6.

MEDLINE=99329089; PubMed=10400701;

Murthy K.K., Clark K., Fortin Y., Shen S.-H., Banville D.;

"ZRP-1, a zyxin-related protein, interacts with the second PDZ domain of the cytosolic protein tyrosine phosphatase hPTP1E.";

J. Biol. Chem. 274:20679-20687(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERACTION WITH NGFR.
MEDLINE=20012928; PubMed=10544233;
Iris S., Hachiya T., Rabizadeh S., Maruyama W., Mukai J., Li Y.,
Reed J.C., Bredesen D.E., Sato T.A.;
"Functional interaction of Fas-associated phosphatase-1 (FAP-1) with
p75 (NTR) and their effect on NF-kappaB activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
MEDLINE=95232528; PubMed=7536343;
Sato T., Irie S., Kitada S., Reed J.C.;
"FAP-1: a protein tyrosine phosphatase that associates with Fas.";
Science 268:411-415(1995).
                                                                                                                                                                                                                                                                                                                                                                                   Wang H.Y.; Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Irie S., Hachiya T., Sato T.A.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
          SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1279-1883 FROM N.A. (ISOFORM 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [10]
INTERACTION WITH PLEKHA1 AND PLEKHA2.
                                                                                                                                                                                               TISSUE-Fibroblast;
MEDLINE-95014139; PubMed=7929060;
                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1216-2490 FROM N.A.
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                                                                                                                                FEBS Lett. 337:200-206(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EBS Lett. 460:191-198(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences."
                                                                                                                                                                           SEQUENCE FROM N.A.
                                rISSUE=Leukemia;
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                                                                                                                                                                                                                                                                                   Kozlov G., Gehring K., Ekiel I., "Solution structure of the PDZ2 domain from human phosphatase hPTP1E and its interactions with C-terminal peptides from the Fas receptor."; Biochemistry 39:2572-2580(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GUANINE NUCLECTIDE EXCHANGE FACTOR RA-GEF-2.

MEDLINES-22039786; PubMed=12035257; DOI=10.1016/S0022-2836(02)00544-2; Kozlov G., Banville D., Gehring K., Ekiel I.; 1016/S0021-2836(02)00544-2; Solution structure of the PDZ2 domain from cytosolic human phosphatase hPTPIE complexed with a peptide reveals contribution of the beta2-beta3 loop to PDZ domain-ligand interactions."; Mol. Biol. 320:813-820(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Hum. Genet. 47:614-61912002).
-!- FUNCTION: Regulates negatively FAS-induced apoptosis and NGFR-mediated pro-apoptotic signaling.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yoshida S., Harada H., Nagai H., Fukino K., Teramoto A., Emi M.; "Head-to-head juxtaposition of Fas-associated phosphatase-1 (FAP-1) and c-Jun NH2-terminal kinase 3 (JNK3) genes: genomic structure and seven polymorphisms of the FAP-1 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exception
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
-!- SIMILARITY: Contains 1 FERM domain.
-!- SIMILARITY: Contains 5 PDZ/DHR domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF.
                                                                                                                                                                             STRUCTURE BY NMR OF 1361-1456 UNCOMPLEXED AND IN COMPLEX WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO-1419 AND MET-1522.
22323362; PubMed=12436199; DOI=10.1007/s100380200094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C-TERMINUS
Kimber W.A., Deak M., Prescott A.R., Alessi D.R.;
"Interaction of the protein tyrosine phosphatase PTPL1 with
PtdIns (3,4) P2-binding adaptor protein TAPP1.";
Biochem. J. 376:55-535 (2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR OF 1361-1456 IN COMPLEX WITH THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and PLEKHA2 through its first PDZ domain. SUBCELLULAR LOCATION: Cytoplasmic (By sim ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q12923-2; Sequence=VSP_000496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q12923-3; Sequence=VSP_000497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q12923-1; Sequence=Displayed;
                                                                                                                                                                                                               C-TERMINUS OF TNFRSF6.
MEDLINE=20170882; PubMed=10704206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U12128; AAB60339.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22323362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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D21210; BAA04751.1; -D21211; BAA04752.1; -X80289; CAA56563.1; -X79676; CAA56124.1; -

BAA04750.1;

D21209; E D21210; E D21211; E

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initiative."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 QIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 MVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFTVRVF
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MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsleh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 GVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVL 232
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Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.3%; Score 592.5; DB 1; Length 2485; 47.6%; Pred. No. 1e-47;
                                                                                                                                                                                                                                                                                                                                       MIM; 600267; -.
GO; GO:0004725; F:protein-tyrosine-phosphatase activity; TAS.
GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
Interpro; IPR000299; Band 4.1.
Interpro; IPR009065; FERM.
Interpro; IPR011009; Kinase_like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR01199; PDZ.
InterPro; IPR011036; PH related.
InterPro; IPR010387; TYR_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000387; TYR_phosphatase.
Prom; Pr00123; Phosphatase; 1.
Prints; Pr00102; Y_phosphatase; 1.
PRINTS; PR001707; PRTPHPHTASE.
PROSITE; PS00660; PERM_1; FALSE_NEG.
PROSITE; PS00660; PERM_2; FALSE_NEG.
PROSITE; PS00661; PERM_2; FALSE_NEG.
PROSITE; PS00661; PERM_2; FALSE_NEG.
PROSITE; PS00661; PERM_2; FALSE_NEG.
PROSITE; PS00661; PERM_2; TYR_PROSITE; PS00183; TYR_PHOSPHATASE_1; FALSE_NEG.
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            L34583; AAC41755.1; -.
AF233323; AAF63474.1; -.
BC039610; AAH39610.1; ALT_TERM.
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                                                                                                           PIR, A54971; A54971.
PIR, 167629; 167629.
PIR, 167630; 167630.
PIR, 107630; 167630.
PIR, 107630; NMR, A=1367-1456.
PDB; 107X; NMR, A=1357-1456.
PDB; 3PDZ; NMR, A=1367-1456.
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Matches 111; Conservative
                                                                                                                                                                                                                                                                                                    Genew; HGNC:9646; PTPN13.
MIM; 600267; -.
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                      EMBL;
EMBL;
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Q6GPK7
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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W. Ilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Richardiguez A.C., Grimmood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE ACCOVERS.

A Klein S., Strausberg R.;

Klein S., Strausberg R.;

Submitted (UNN-2004) to the EMBL/GenBank/DDBJ databases.

L. SIMILARITY: Contains 1 PDZ/DHR domain.

R EMBL; BC073110; AAH73110.1; -.

R InterPro; IPR001299; Band 4.1.

R InterPro; IPR0019065; FERN.

R InterPro; IPR0019065; FERN.

R InterPro; IPR0019065; FERN.

R InterPro; IPR0019065; PH related.

R InterPro; IPR0019059; PH related.

R InterPro; IPR0019059; PH related.

R InterPro; IPR0019059; PH related.

R InterPro; IPR0019059; PH related.

R InterPro; IPR0019059; PH related.

R InterPro; IPR000190; TYR_phosphatase.

R Pfam; PF00101; Y_phosphatase; 1.

R Pfam; PF00101; Y_phosphatase; 1.

R PRINTS; PR00651; ERMFAMILY.

R PRINTS; PR00601; PRTYPHPHTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 920;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              920 AA; 105109 MW; 8F0BB89C359CD41E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Best Local Similarity 43.5%; Pred. No. 2.9e-40;
Matches 104; Conservative 33; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00404; PTPC_motif; 1.
PROSITE; PS00606; FERM 1; UNKNOWN_1.
PROSITE; PS00067; FERM 3; 1.
PROSITE; PS00016; PDZ; 1.
PROSITE; PS000183; TYR_PHOSPHATASE_1; 1.
PROSITE; PS000183; TYR_PHOSPHATASE_2; 1.
PROSITE; PS00056; TYR_PHOSPHATASE_PTP; 1.
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SMART; SM00228; PDZ; 1.
SMART; SM00194; PTPC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Protein-tyrosine phosphatase H1) (PTP-H1)
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                                                                                                                                                                                                                                                                                                           Yachi A.;
                                                                                                                                                                                                                                         colon.
TCAQFWQVVWDQKLSLIVMLTTLTERGRIKCHQYWP---DPPDVMNHGGFHIQCQSEDCT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 ÖNLDKNRYKDVLPYDTTRVLLQGNEDYINASYVNMEIPPAANLVNK-----YIATQGPLPH 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 QYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHI-TGPLLV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 IAYVSREMLVTNTQTGEEHTVTHLQYVAWPDHGVPDDSSDFLEFVNYVRSLRVDSEPVLV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLE 230
790 YVFREMLLTDTETGDEFPIIHLQYVAWPDHGVPDDSSDFLEFATYVRQKRMENQPVLVHC 849
                                  SAGVGRIGVFICVDVVFSALEKNYSFDIMNIVTOMRKORCGMIQIKEOYQFCYEIVLEV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYI-----RIVNHEEEYFYIATQGPLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 TIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEH--FSVFLETFHVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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                                                                                                                                                                                                                                                                                            GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA. GO; GO:0006470; P:protein amino acid dephosphorylation; IEA. InterPro; IPR000387; TYR phosphatase.
InterPro; IPR00242; TYR phosphatase.
Pfam; PF00102; Y. Phosphatase; 1.
PRINTS; PR00700; PRTYPHPHTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85; Indels
                                                                                                                                                                                                                                                Strausberg R.; Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC033716; AAH33716.1; -GO; GO:0016787; F:hydrolase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   292 AA; 33121 MW; 54B838BDD41D1BD7 CRC64;
                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.9%; Score 500; DB 2; 42.0%; Pred. No. 6.5e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    913 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38; Mismatches
                                                                                                                                                                                                                                                                                                                                                             SMART; SM0194; PTPC; 1.
PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR PHOSPHATASE 2; 1.
PROSITE; PS50055; TYR PHOSPHATASE PTP; 1.
                                                                                                                        Created)
                                                                                                                                                       Hypothetical protein (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Hypothetical protein.
                                                                                                                      01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102; Conservative
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                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLQ 233
                                                                                                                                                                                                                                      TISSUE=Kidney;
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P26045;
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                            Q8N4S3;
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ID PTN3_HU
AC P26045;
DT 01-MAY-
DT 01-MAY-
DT 05-MAY-
DT 05-JUE-
DE Proteir
                                                                                                  Q8N4S3
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                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDINE=91296738; PubMed=1648725;
Yang Q., Tonks N.K.;
"Isolation of a cDNA clone encoding a human protein-tyrosine
phosphatase with homology to the cytoskeletal-associated proteins band
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB=Colon;
MEDLINE=92327504; PubMed=1626183;
Arimura Y., Hinoda Y., Itoh F., Takekawa M., Tsujisaki M., Adachi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytoskeleton.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Expression of cytoskeletal-associated protein tyrosine phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tyrosine + phosphate.
-- SUBCELLULAR LOCATION: Cytoplasmic.
-- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
-- Non-receptor class subfamily.
-- SIMILARITY: Contains 1 FERM domain.
-- SIMILARITY: Contains 1 PDZ/DHR domain.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Imai K., Yachi A.;
"CDNA cloning of new protein tyrosine phosphatases in the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTPHI mRNA in human hepatocellular carcinoma.";
J. Gastroenterol. 29:727-732(1994).
-!- FUNCTION: May act at junctions between the membrane and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0004725; F:protein-tyrosine-phosphatase activity; TAS. GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ikuta S., Itoh F., Hinoda Y., Toyota M., Makiguchi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                         4.1, ezrin, and talin.";
Proc. Natl. Acad. Sci. U.S.A. 88:5949-5953(1991).
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InterPro; IPR000798; Ez/rad/moesin.
InterPro; IPR0004065; FERM.
InterPro; IPR001479; PDZ.
InterPro; IPR0011036; PH_related.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_PP.
Pfam; PP00373; Band 41; 1.
Pfam; PP00595; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 899-913 FROM N.A. MEDLINE=95179278; Pubmed=7874267;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour Biol. 13:180-186(1992).
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EMBL; S39392; AAB22439.2; -...
EMBL; S76309; AAB33583.1; -...
PIR; A41109; A41109.
HSSP; P18031; 1C88.
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MIM; 176877; -.
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SMART; SM00228; PDZ; 1.
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PTNS HUMAN
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SEQUENCE
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PINS HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 TIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEH--FSVFLETFHVT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 OYFTVRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHI-TGPLLV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   841 HCSAGIGKTGVLVTMETAMCLTERNLPIYPLDIVRKWRDQRAMMVQTSSQYKFVCEALLR 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  669 QNLDKNRYKDVLPYDTTRVLLQGNEDYINASYVNMEIFAANLVNK-----YIATQGPLPH 723
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Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: Contains 1 PDZ/DHR domain.
EMBL; AF106702; AAD22773.1; -.
HSSP; P11171, IGG3.
MGD; MG1:1099792; Ptpn4.
GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. . .; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ONRDKANRYRDILPYDSTRVPLGKAKDYINASYI-----RIVNHEEEYFYIATOGPLPE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               724 ICAQEWQVVWDQKLSLIVMLTTLTERGRIKCHQYWP---DPPDVMNHGGFHIQCQSEDCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=20510023; PubMed=11054567;
Park K.W., Lee B.J., Lee S.H., Lee J.E., Choi E.Y., Kim B.J.,
Hwann R., Park K.A., Baik J.H.;
"Molecular cloning and characterization of a protein tyrosine
phosphatase enriched in testis, a putative murine homologue of human
                                                                                                                                                                                                                                                                                                                                                                                           18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laus musocuras, vacobe;
Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                          Cytoskeleton, Hydrolase, Protein phosphatase, Structural protein.
DOMAIN 29 312
                                                                                                                                                                                                                              Protein-tyrosine phosphatase.
Phosphocysteine intermediate (By
similarity).
1; 29A539ACDE2F1515 CRC64;
                                                                                                                                                                                                                                                                                                                                         tch 39.8%; Score 499; DB 1; Length 913; al Similarity 42.0%; Pred. No. 3.3e-39; 102; Conservative 38; Mismatches 85; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.1-NOV-1999 (TrEMBLrel. 12, Created)
1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
0.1-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Testis-enriched protein tyrosine phosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   926 AA
PROSITE; PS00660; FERM_1; 1.
PROSITE; PS00661; FERM_2; 1.
PROSITE; PS50106; PDZ, 1.
PROSITE; PS50106; PDZ, 1.
PROSITE; PS50038; TYR PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR_PHOSPHATASE 2; 1.
PROSITE; PS50056; TYR_PHOSPHATASE 2; 1.
                                                                                                                                                                                                                                                                                                     913 AA; 104029 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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842
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54 TIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQ- 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96102179; PubMed=8524829; Streuli M.; Pulido R., Serra-Pages C., Tang M., Streuli M.; Putlido R., Serra-Pages C., Tang M., Streuli M.; AnskPtp delta/PTP sigma subfamily of transmembrane protein-tyrosine-phosphatases: multiple human LAR, PTP delta, and PTP sigma isoforms are expressed in a tissue-specific manner and associate with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 LVHCSAGVGRTGVFICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tch 39.4%; Score 493.5; DB 2; Length 926; al Similarity 41.2%; Pred. No. 1.1e-38; 101; Conservative 43; Mismatches 80; Indels 21.
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PROSITE; PS00661; FERM 2; 1.
PROSITE; PS50057; FERM 3; 1.
PROSITE; PS50106; PDZ; 1.
PROSITE; PS60108; TYR PHOSPHATASE 1; 1.
PROSITE; PS50056; TYR PHOSPHATASE 2; 1.
PROSITE; PS50055; TYR PHOSPHATASE 2; 1.
                                                 InterPro; IPR009065; FERM.
InterPro; IPR001478; PDZ.
InterPro; IPR011036; PH related.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_P.
Pfam; PF00373; Band 41; I.
Pfam; PF00595; PDZ; 1.
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                  InterPro; IPR000798; Ez/rad/moesin.
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BAND41.
                                                                                                                                                                                                                                                            Pfam, PF00102; Y phosphatase, 1 PRINTS; PR00935; BAND41. PRINTS; PR00661; ERMFAMILY. PRINTS; PR00700; PRTYPHPHTASE. SMART; SM00295; B41; 1. SMART; SM0228; PDZ; 1.
Band 4.1
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InterPro; IPR000299;
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EMBL, U40317; AAC50567.1; -.
EMBL, AC005790; AAC62832.1; -.
EMBL, AC005338; AAC27825.1; -.
EMBL, AC005788; AAC62834.1; -.
EMBL; S78080; AAB21146.2; -.
HSSP; P10586; ILAR.
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Carimwood J., Gordon L.A., Olsen A.S., Terry A., Schmutz J.,

Lamerdin J.E., Hellsten U., Goodstein D., Couronne O., Tran-Gyamfi M.,

A marts A., Altherr M., Ashworth L., Bajorek E., Black S., Branscomb E.,

A caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M.,

A Caenepeel S., Carrano A.V., Caoile C., Chan Y.M., Christensen M.,

A Caenepeel S., Flowers D., Fotopulos D., Dahal P., Danys M., Detter J.C.,

B Secobar J., Flowers D., Fotopulos D., Garcia C., Georgescu A.M.,

A Baydu L., Ho I., Hang W., Israni S., Jett J., Ramer N., Hawkins T.,

A Haydu L., Ho I., Hang W., Israni S., Jett J., Radher K., Kimball H.,

A Cobayashi A., Larionov V., Leem S.-H., Lopez F., Lou Y., Lowry S.,

A Malfatti S., Martinez D., McCready P.M., Medina C., Morgan J.,

A Ropkie A.P., Predki P., Quan G., Ramirez L., Rash S., Retterer J.,

R Rodriguez A., Rogers S., Salamov A., Salazar A., She X., Smith D.,

A Slezak T., Solovyev V., Thayer N., Tice H., Tsai M., Ustaszewska A.,

R Storey T.S., DeJong P., Dickson M., Gordon D., Eichler E.E.,

R Pennacchio L.A., Richardson P., Stubbs L., Rokhsar D.S., Myers R.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERACTIONS WITH PPFIAL; PPFIAZ AND PPFIAZ.
MEDILINE=98288299; PubMed=9624153;
Serra-Pages C., Medley Q.G., Tang M., Hart A., Streuli M.;
"Lippins, a family of LAR transmembrane protein-tyrosine phosphatase-interacting proteins.";
J. Biol. Chem. 273:15611-15620(1998).
-!- FUNCTION: Interacts with LAR-interacting protein LIP.1.
-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)0 = protein
                                                                                      R., Rodan G.A., Schmidt A.;
1: alternative splicing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1503-1589 FROM N.A.
MEDLINE=92119637; PubMed=1370651;
Adachi M., Sekiya M., Arimura Y., Takekawa M., Itoh F., Hinoda Y.,
Imai K., Yachi A.;
"Protein-tyrosine phosphatase expression in pre-B cell NALM-6.";
Cancer Res. 52:737-740(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q13332-3; Sequence=VSP_050022, VSP_050026, VSP_050027;
Name=PTPS-MEC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs to the protein-tyrosine phosphatase family
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TISSUE SPRCIFICITY: Detected in all tissues tested except for placenta and liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Contains 8 fibronectin type III domains.
-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rubin E.M., Lucas S.M.; "The DNA sequence and biology of human chromosome 19.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tyrosine + phosphate.
SUBUNIT: Interacts with PPFIA1, PPFIA2 and PPFIA3
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
the LAR-interacting protein LIP.1.";
Proc. Natl. Acad. Sci. U.S.A. 92:11686-11690(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=5;
Comment=Additional isoforms seem to exist;
                                                                   MEDLINE=96255038; PubMed=8992885;
Endo N., Rutledge S.J., Opas E.E., Vogel R.
"Human protein tyrosine phosphatase-sigma:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q13332-4; Sequence=VSP_050024;
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                                                                                                                          inhibition by bisphosphonates.";
J. Bone Miner. Res. 11:535-543(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor class 2A subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 428:529-535(2004).
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N-linked (GloMAc. . .) (Potential)
N-linked (GloMAc. . .) (Potential)
N-linked (GloMAc. . .) (Potential)
N-linked (GloMAc. . .) (Potential)
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The developing leech by specific central neurons as well as select

RT peripheral neurons, muscles, and other cells.",

DR Neurosci. 18:2391-3002(1998).

BR HSSP; PROSSI; PRO201-3002(1998).

R HSSP; PROSSI; PRO201-3002(1998).

R HSSP; PROSSI; PRO201-3002(1998).

R GO; GO:0006787; Preceptor activity; IEA.

GO; GO:0004725; Preceptor activity; IEA.

GO; GO:0004725; Preceptor activity; IEA.

GO; GO:0004725; Preceptor activity; IEA.

GO; GO:0004725; Preceptor activity; IEA.

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GO; GO:0004725; Preceptor activity; IEA.

GO; GO:0004725; Preceptor activity; IEA.

GO; GO:0004725; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PRO2016; PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLBFBHFSVF-LETFHVTQYFT 115
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Blasmobranchii, Squalea, Hypnosqualea, Pristiorajea, Batoidea,
Myliobatiformes, Myliobatoidei, Potamotrygonidae, Potamotrygon.

NCBI_TaxID=86373,
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Best Local Similarity 41.1%; Pred. No. 1.4e-37;
Matches 99; Conservative 45; Mismatches 82; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2051 AA; 229604 MW; D60F8A032F659B00 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 24, Last annotation update)
RyPTPRZAC protein (Fragment).
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                                                                                                                           Missing (In isoform PTPS-F4-7).

| FIId=VSP 050023. |
| Missing (In isoform PTPS-F4-7). |
| FTId=VSP 050024. |
| FTId=VSP 050024. |
| V -> I (In isoform PTPS-F4-7). |
| FTId=VSP 050025. |
| Missing (In isoform PTPS-MEB). |
| FTID=VSP 050026. |
| S-> G (in isoform PTPS-MEB). |
| FTID=VSP 050026. |
| FTID=VSP 050026. |
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NCBI_TaxID=6421;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.0%; Score 488.5; DB 1; Length 1948; 41.9%; Pred. No. 8.6e-38;
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ZeguENCE FROM N.A.
BEDINE=98195364; PubMed=9526016;
Gershon T.R., Baker M.W., Nitabach M., Wu P., Macagno E.R.;
                                                                    fissing (In isoform PTPS-MEB).
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 8.6e-38; 45; Mismatches 80
                                       /FTId=VSP 050021
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                                                             MEDLINE=20219325; PubMed=10754074; Ono-Koyanagi K., Suga H., Katch K., Miyata T.; Ono-Koyanagi K., Suga H., Katch K., Miyata T.; Protein tyrosine phosphatases from amphioxus, hagfish, and ray: alvergence of tissue-specific isoform genes in the early evolution of
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TJW-2003 (TrEMBLrel. 24, Last annotation update)
01-0TW-2003 (TrEMBLrel. 24, Last annotation update)
Receptor protein tyrosine phosphatase CRYP-alpha (Fragment).
Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
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Johnson K.G., Holt C.E.;
"Expression of CRYP-alpha, LAR, PTP-delta, and PTP-rho in the
developing Xenopus visual system.";
Mech. Dev. 92:291-294(2000)
                                                                                                                                                                                                                                                                                                                                                       Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB033586; BAA95193.1; -.
G0; 0G0:0016787; F:hydrolase activity, IEA.
G0; G0:0004725; F:protein tyrosine phosphatase activity, IEA.
G0; G0:0006470; P:protein amino acid dephosphorylation; IEA.
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InterPro; IPR000242; TYR_PP.
Pfam, PF00102; Y_phosphatase, 2.
PRINTS; PR007100; PRTYPHPHTASE.
SWART; SW00194; PTPC; 2.
PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
PROSITE; PS50055; TYR_PHOSPHATASE 2; 2.
PROSITE; PS50055; TYR_PHOSPHATASE 2; 2.
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Matches 100; Conservative
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NCBL_TaxID=8355;
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MEDLINE=20219325; PubMed=10754074;
MCDLINE=20219325; PubMed=10754074;
Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
"Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
"Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
divergence of tissue-specific isoform genes in the early evolution of
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Elasmobranchii, Squalea, Hypnosqualea, Pristiorajea, Batoidea,
Myliobatiformes, Myliobatoidei, Potamotrygonidae, Potamotrygon.
            R GO; GO: 0016797; F:hydrolase activity; IEA.

R GO; GO: 0016725; F:protein tyrosine phosphatase activity; IEA.

R GO; GO: 0004872; F:protein tyrosine phosphatase activity; IEA.

R GO; GO: 0006470; F:receptor activity; IEA.

R InterPro; IPR000387; TYR_phosphatase.

R InterPro; IPR000342; TYR_phosphatase.

R PRINTS; PR00102; Y_phosphatase; 2.

R PRINTS; PR00100; PRTYPHPHTASE.

R SMART; SM00194; PTPC; 2.

R PROSITE; PS00083; TYR_PHOSPHATASE 1; 2.

R PROSITE; PS00085; TYR_PHOSPHATASE 2; 2.

R PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
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EMBL, ABG33584; BAA95191.1; -.
GO: GO:0016787; F:hydralase activity; IEA.
GO: GO:0004725; F:protein tyrosine phosphatase activity; IEA.
GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
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larity 41.5%; Pred. No. 4.1e-38;
Conservative 46; Mismatches 80
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Best Local Similarity
Matches 100; Conserv
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P10586; 1LAR
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57 DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVF-LETFHVTQYFT 115
                                                                                                                                                                                                                                                                                                                                                                                                              283 DFWRMLWEHNSTIVVWLTKLREMGREKCHQYWP--AERSARYQYFVVDPWAEYNWPQYI- 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400 CSAGVGRIGVFITLSIVLERMRYEGVVDIFQTVKMLRTQRPAMVQTEDQYQFCYRAALEY 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 VRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSH----ITGPLLVH 171
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                                                                                                                                                                                                                                                                                                             2 NRDKNRYRDILPYDSTRVPLG----KNKDYINASYIRIVNHEEEYFYIATQGPLPETIE 56
                                                                                                                                                                                                                                 Query Match 38.7%; Score 484.5; DB 2; Length 468;
Best Local Similarity 41.9%; Pred. No. 3.7e-38;
Matches 101; Conservative 44; Mismatches 81; Indels 15; Gaps
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_PP.
Pfam; PF00102; Y_phosphatase; 2.
PRINTS; PR001709; PRTYPHPHTASE.
SMART; SM00194; PTPC; 2.
ROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
RPOSITE; PS50055; TYR_PHOSPHATASE_1; 2.
RPOSITE; PS50055; TYR_PHOSPHATASE_2; 2.
RHOALDASE.
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I SSRQÜENCE 468 AA; 53885 MW; 8BICABEOBE9692E4 CRC64;
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GenCore version 5.1.6
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Run on:

of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

283416 seqs, 96216763 residues

Total number Searched:

283416

PIR 79:*
1: pir1:*
2: pir2:*
1: pir3:*
: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

leukocyte antigen-	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein tyrosine p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p
846216	A60345	S14294	A33899	I58345	817669	A57064	860613	S17670	I49372	JC2366	868250	A53661	S51005	I38140	JW0049
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36.8	36.7	36.6	36.6	36.6	36.6	36.5	36.5	36.5	36.4	36.2	36.2	36.2	36.1	36.0	35.9
460.5 36.8	460 36.7	459 36.6	459 36.6	458.5 36.6	458 36.6	457 36.5	457 36.5	457 36.5		454 36.2	453 36.2	453 36.2		451.5 36.0	

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Syl625 RESULT 2

A, Molecule type: mRNA

H

phosphatase containing a membrane

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A;Cross-references: UNIPROT:Q12923; GB:D21211; NID:g452193; PIDN:BAA04752.1; PID:g452194 C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology; C;Keywords: phosphoric monoester hydrolase F;574-868/Domain: protein 4.1 membrane-binding domain homology <B41> F;1182-1258/Domain: GLGF domain homology <GGG2> F;2046-2265/Domain: protein-tyrosine-phosphatase homology <PTP>
C,Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004 C,Accession: I67630
R;Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S. FEBS Lett. 337, 200-206, 1994
A;Title: Molecular cloning of a novel protein-tyrosine phosphatase containin A;Reference number: IS3483; MUID:94116679; PMID:8287977
A;Accession: I67630
                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2294 <RES>
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Best Local Similarity 47.6'
Matches 111; Conservative
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F;1089-1165/Domain: GLGF domain homology <GLG1>
F;1361-1437/Domain: GLGF domain homology <GLG2>
F;1495-1574/Domain: GLGF domain homology <GLG3>
F;1769-1840/Domain: GLGF domain homology <GLG3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: GB:L34581; NID:g806295; PIDN:AAC42055:1; PID:g806296
R;Hendariks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
submittick to the EMBL Data Library, June 1993
A,Description: Assessment of the expression levels of murine protein-tyrosine phosphatas
                                                                                                                                                                  8
                                            A;cross-references: UNIPROT:Q64512; UNIPROT:Q62370; EMBL:D83966; NID:g1232103; PIDN:BAA1
A;Experimental source: strain DBA/2; cell line MEL 745A
R;Wolf, B.B.; Brown, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN13, nonreceptor type 13, splice form 3 C;Species: Homo sapiens (man)
                                                                                                                                                               receptor-bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: Z23059; NID: 9438155; PIDN: CAA80594.1; PID: 9438156
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F;2203-2422/Domain: protein-tyroaine-phosphatase homology <PTD1>
F;2374/Active site: Cys (phosphocysteine intermediate) #status predicted
F;2380/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1329-1354, K',1356-1447, 'R',1449-1454 <RES>
A;Cross-references: GB:L34582; NID:g806297; PIDN:AAC42056.1; PID:g806298
A;Accession: I81209
                                                                                                                                                                                                                                                                                                                                                                                            Fas.
                                                                                                                              FEBS Lett. 376, 177-180, 1995
A;Title: Epidernal growth factor-binding protein activates soluble and A;Reference number: 867987; MUID:96105375; PMID:7498536
A;Accession: 867987
                                                                                                                                                                                                                                         A,Molecule type: protein
A,Residues: 1098-1102 < WOL>
A,Experimental source: submaxillary glands
B,Sato, T., Irie, S., Kitada, S.; Reed, J.C.
Science 268, 411-415, 1995
A,Title: FAP-1: a protein tyrosine phosphatase that associates with la, Reference number: 159595; MUID:95232528; PMID:7536343
A,Accession: 181210
A,Status: preliminary; translated from GB/EMBL/DDBJ
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A,Residues: 1338-1354,'K',1356-1447,'R',1449-1454 <RE2>
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A,Molecule type: mRNA
A,Residues: 2266-2372
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R.Mackwa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
FEBS Lett. 337, 200-206, 1994
FEBS Lett. 337, 200-206, 1994
A.Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membran A.Reference number: 153483; MUID:94116679; PMID:8287977
A.Accession: 167629
A.Accession: 167629
A.Accession: 167629
A.Molecula type: mRNA
A.Residues: 1-2466 A.RES>
A.Across-references: UNIPROT:012923; GB:D21210; NID:9452191; PIDN:BAA04751.1; PID:9452192; C.Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology: C.Keywords: phosphoric monoester hydrolase
F.F374-868 Domain: protein 4.1 membrane-binding domain homology cB41>
F.1354-1430/Domain: grotein-tyrosine-phosphatase homology <AGG2>
F.218-2437/Domain: protein-tyrosine-phosphatase homology <PTP>
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C.Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C.Accession: I67629
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47.3%; Score 592.5; 47.6%; Pred. No. 1.3
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A,Cross-references: UNIPROT:P26045; GB:M64572; NID:9179912; PIDN:AAA35647.1; PID:9179912
R;Ikuta, S.; Itoh, F.; Hinoda, Y.; Toyota, M.; Makiguchi, Y.; Imai, K.; Yachi, A.
G. Gastrocenterol. 29, 772-732, 1994
A;Title: Expression of cytoskeletal-associated protein tyrosine phosphatase PTPH1 mRNA i
A;Reference number: 155698; MUID:95179278; PMID:7874267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Map position: 9431-9431
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; I
C;Superfamily: protein-tyrosine-phosphoric monoester hydrolase; tyrosine-specific phosphatas
F;31-308/Domain: protein 4.1 membrane-binding domain homology <B41>
F;516-590/Domain: GLGF domain homology <GLG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 88, 5949-5953, 1991
A;Title: Isolation of a cDNA clone encoding a human protein-tyrosine phosphatase with hc
A;Reference number: A41109; MUID:91296738; PMID:1648725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - human
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MYLENNCNVIAMITREIECGVIKCYSYMPISL-KEPLEFEHFSVFLETFHVTQYFTVRVF 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 27-Mar-1992 #sequence_revision 02-May-1994 #text_change 09-Jul-2004
C;Accession: A41109; I55698
R;Yang, Q;; Tonks, N.K.
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A,Residues: 899-913 <RES>
A,Cross-references: GB:S76309; NID:g913165; PIDN:AAB33583.1; PID:g913166
                                                                                                                                                                                                                                                                                                  predicted
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2.2e-38;
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39.8%; Score 499; UB
Best Local Similarity 42.0%; Pred. No. 2.2e
Matches 102; Conservative 38; Mismatches
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A; Residues: 1-913 < YAN>
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                                                                                                                                                                                                                                                                                     protein-tyrosine-phosphatase (EC 3.1.3.48) PTPNI3, nonreceptor type 13, splice form 1 [V N,Alternate names: Fas-associated phosphatase FAP-1; protein-tyrosine-phosphatase hPTPIE C;Species Homo sapiens (man) C;Species Homo sapiens (man) C;Date: 11-Nov-1994 #sequence revision 08-Feb-1996 #text_change 09-Jul-2004 C;Date: 11-Nov-1994 #sequence revision 08-Feb-1996 #text_change 09-Jul-2004 C;Date: 11-Nov-1994 #sequence revision 08-Feb-1996 #text_change 09-Jul-2004 C;Date: 11-Nov-1994 #sequence revision 08-Feb-1996 #text_change 09-Jul-2004 R;Banville, D: Ahmad, s.; $tccoo. R: She, S.H.

J. Biol. Chem. 269, 22320-22327, 1994
A;Title: A novel protein-tyrosine phosphatase with homology to both the cytoskeletal profession: Ab4971
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Note: sequence shown follows authors' translation at positions 62-63
B;Saras, J.; Claesson-Welsh, L: Heldin, C.H.; Gonez, L.J.
J. Biol. Chem. 269, 24082-24089, 1994
A;Title: Cloning and characterization of PTPL1, a protein tyrosine phosphatase with simit A;Reference number: A55144; MUID:95044139; PMID:792960
A;Accession: A5514
A;Cross-references: GB:X80289; NID:9514139; PMID:7929651; PID:9515031
A;Residues: 1-61, GS, 64-839, 'D', 841-1055,1075-1133, 'FH', 1136-1210, 'I', 1212-1383, 1389-15
A;Cross-references: GB:X80289; NID:9512528; PMID:7536343
A;Reference number: 159595; MUID:95232528; PMID:7536343
A;Reference number: 159595; MUID:95232528; PMID:7536343
A;Reference number: IS9595
A;Reference number: Langled from GB/EMBL/DDBU
A;Reference number: Langled from GB/EMBL/DDBU
A;Reference number: Langled from GB/EMBL/DDBU
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-61, 'GS', '64-839, 'D', 841-1210, 'I', 1212-1383,1389-2299, 'QM', 2302-2490 <RE2>
A; Molecule type: mRNA
A; Residues: 1-61, 'GS', '64-839, 'D', 841-1210, 'I', 1212-1383,1389-2299, 'QM', 2302-2490 <RE2>
C; Genetics:
C; Genetics:
A; Gene: GDB: PTPN13
A; Cross-references: GDB: 306348; OMIM: 600267
A; Map position: 4Q21.3-4Q21.3
C; Superfamily: protein-tyrosine-phosphatase, nonreceptor type 13; GLGF domain homology; C; Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosing; protein-tyrosine-binding domain homology <GLG2>
F; 1039-1175/Domain: GLGF domain homology <GLG2>
F; 1173-1454/Domain: GLGF domain homology <GLG3>
F; 1183-1454/Domain: GLGF domain homology <GLG3>
F; 1199-1870/Domain: GLGF domain homology <GLG3>
F; 1193-1870/Domain: GLGF domain homology <GLG3>
F; 1193-1870/Domain: protein-tyrosine-phosphatase homology <FTP1>
F; 12413/Active site: Cys (phosphocysteine intermediate) #status predicted
F; 2419/Binding site: substrate phosphate (Arg) #status predicted
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A; Residues: 1279-1888 KES>
A; Cross-references: GB:L34583; NID:g806291; PIDN:AAC41755.1; PID:g806292
R; Maekawa, K.; Imagawa, N.; Nagamatsu, M.; Harada, S.
R; BES Lett. 337, 200-206, 1994
A; Title: Molecular cloning of a novel protein-tyrosine phosphatase containing a membrane
A; Reference number: IS3483; MUID:94116679; PMID:8287977
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             TLEDIQTREVRHISHLNFTAWPDHDTPSQPDDLLTFISYMRHIHRSGPIITHCSAGIGRS 2396
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46.8%; Pred. No. 7.8e-46;
iive 43; Mismatches 80;
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protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type J precursor - human NyAlternate names: density enhanced phosphatase-1 (DEP-1); protein-tyrosine phosphatase C;Species: Homo sapiens (man) C;Date: 01-Mar-1996 #sequence_revision 08-Mar-1996 #text_change 09-Jul-2004 C;Accession: 138670; 152599 R;Ostman, A.; Yang, Q.; Tonks, N.K. Proc. Natl. Acad. Sci. U.S.A. 91, 9680-9684, 1994 A;Title: Expression of DEP-1, a receptor-like protein-tyrosine-phosphatase, is enhanced A;Reference number: 138670; MUID:95024024; PMID:7937872
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A;Residues: 1-216, 'IngVRKAA', 225-260, 'G', 262-285, 'GTEGGLDASNTERSRA', 302,'S', 304,'TAEVHD
A;Cross-references: GB:D37781; NID:g633072; PIDN:BAA07035.1; PID:g633073
C;Comment: Enhanced expression of this protein with increasing cell density suggests a
C;Genetics:
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C, Function:
A, Map position: 1943.4-1943.4

C, Function:
A, Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine and C, Superfamily: protein-tyrosine-phosphatase, receptor type J; fibronectin type III repet C, Superfamily: protein-tyrosine-phosphoric monoester hydrolase; receptor; train F; 1-35/Domain: signal sequence #status predicted <SIG-P, 1-35/Domain: signal sequence #status predicted <SIG-P, 1-35/Domain: fibronectin type III repeat homology <3FNA-F; 1-35/Domain: fibronectin type III repeat homology <3FNB-F; 1-35/Domain: fibronectin type III repeat homology <3FNB-F; 1-35-445/Domain: fibronectin type III repeat homology <3FNB-F; 1-35-445/Domain: fibronectin type III repeat homology <3FNB-F; 1-35-617/Domain: fibronectin type III repeat homology <3FNB-F; 1-35-617/Domain: fibronectin type III repeat homology <3FNB-F; 1-35-617/Domain: fibronectin type III repeat homology <3FNB-F; 1-35-35/Domain: fibronectin type III
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A,Residues: 1-1337 CRSS-
A,Festidues: 1-1337 CRSS-
A,Cross-references: UNIPROT: 012913; EMBL: U10886; NID: 9558754; PID: 9558755
A,Experimental source: HeLa cells
R;Honda, H.; Inazawa, J.; Nishida, J.; Yazaki, Y.; Hirai, H.
Blood 84, 4186-4194, 1994
A;Title: Molecular cloning, characterization, and chromosomal localization of a novel
A,Reference number: 152599; MUID: 95086212; PMID: 7994032
A,Stcession: I22599
A,Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                     TIEDFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQY 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 LVHCSAGVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIV
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                                                                                           Gaps
                                                                                  21;
    Length 926;
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    38.0%; Score 476.5; DB 1
40.8%; Pred. No. 2.9e-36;
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                                                                                  100; Conservative 39; Mismatches
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A,Cross-references: GDB:385040; OMIM:600925
                                           Similarity
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Query Match
Best Local S:
Matches 100
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A,Residues: 1-2051 <GER>
A,Cross-references: UNIPROT:044328; EMBL:AF017083; NID:g2695654; PID:g2695655; PIDN:AAB9
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 20-Mar-1992 #sequence_revision 02-May-1994 #text_change 09-Jul-2004
C;Accession: A41105 # Warshawsky, I.; Majerus, P.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 5867-5871, 1991
A;Title: Identification, cloning, and expression of a cytosolic megakaryocyte protein-ty A;Reference number: A41105; MUID:91288564; PMID:1648233
A;Accession: A41105
A;Accession: A41105
A;Residues: 1-926 <GGA>
A;Molecule type: mRNA
A;Residues: 1-926 <GGA>
A;Molecule type: mRNA
A;Accession: MIPROT:P29074; GB:M68941; NID:g190747; PIDN:AAA36530.1; PID:g190748
A;Accession: GB:PPPNA
A;Gene: GB:PPPNA
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A)Map position: 9931-9931
C)Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; pt C; Superfamily: protein-tyrosine-phosphatase, noncester hydrolase; tyrosine-specific phosphatase
C; Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
F; 31-308/Domain: protein 4.1 membrane-binding domain homology cB41>
F; 523-597/Domain: GLGF domain homology cGGA>
F; 573-90/Domain: protein-tyrosine-phosphatase homology cPTP>
F; 852/Active site: Cys (phosphocysteine intermediate) #status predicted
F; 858/Meinding site: substrate phosphate (Arg) #status predicted
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A;Gene: LAR2
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
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                                                                                                                                               Cypectable intuction wedicturate (wedictured therein)

Cybate: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

Cybate: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

Cybate: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

Rydershon, TR.; Baker, M.; Nitabach, M.; Wu, P.; Macagno, E.R.

A;Description: Two receptor tyrosine phosphatases of the LAR subfamily are expressed a;Rydersence number: 220939

A;Reference number: 220939

A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein-tyrosine-phosphatase (BC 3.1.3.48) PTPN4, nonreceptor type 4 [validated]
N/Alternate names: PTPase MEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1983 CSAGVGRTGVFITLSIVLERMRFEGAVDVFQTVNVLRTQRPGMVQTEEQYARCYRAALEY 2042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVF-LETFHVTQYFT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 CSAGVGRIGVFICVDVVFSALEXNYSFDIMNIVIQMRKQRCGMIQTKEQYQFCYEIVLEV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26
                                                                              receptor tyrosine phosphatase - medicinal leech
C;Species: Hirudo medicinalis (medicinal leech)
C;Date: 22-Oct_1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 NRDKNRYRDILPYDSTRVPLG----KNKDYINASYIRIVNHEEEYFYIATQGPLPETIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 486.5; DB 2; Length 2051;
; Pred. No. 8.7e-37;
45; Mismatches 82; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity 41.19
99; Conservative
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Best Local S:
Matches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116
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231

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A;Molecule type: mRNA
A;Residues: 1-1907 cMAG>
A;Residues: 1-1907 cMAG>
A;Cross-references: UNIPROT:Q64494; EMBL:X82288; NID:g587483; PIDN:CAA57732.1; PID:g5874
R;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
submitted to the EMBL Data Library, June 1993
A;Description: Assessment of the expression levels of murine protein-tyrosine phosphatas
A;Reference number: 340280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Wagner, J.; Boerboom, D.; Tremblay, M.L.
Biochem. 226, 773-782, 1994
A;Title: Molecular cloning and tissue-specific RNA processing of a murine receptor-type A;Reference number: 850893; MUID:95112841; PMID:7529177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Molecule type: mRNA
A,Residues: 1441-1501, E',1503-1546 <HEN>
A;Cross-references: EMBL:223050; NID:g438137; PIDN:CAA80585.1; PID:g438138
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type sigma precursor - mouse C;Species: Mus musculus (house mouse)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
   DFWRALWENNSTIVVWLTKLREMGREKCHQYWP--AERSARYQYFVVDPMAEYNMPQYI- 1372
                                                                                                                                                                                                                                                                                                          1373 LREFKVTDARDGOŚRTVROFOFTDWPEQGAPKSGEGFIDFIGOVHKTKEQFGQDGPISVH 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1722 DFWRALWENNSTIVVMLTKLREMGREKCHQYWP--AERSARYQYFVVDPMAEYNMPQYI- 1778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1664 NKFKNRLVNILPYESSRVCLQPIRGVEGSDYINASFID--GYRQQKAYIATQGPLAETTE 1721
                                                                                                            DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVF-LETFHVTQYFT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVF-LETFHVTQYFT 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transigly-copy and an immunoglobulin homology simml.
F; 246-209/Domain: immunoglobulin homology simml.
F; 246-300/Domain: immunoglobulin homology simml.
F; 246-300/Domain: immunoglobulin homology simml.
F; 246-300/Domain: fibronectin type III repeat homology simml homology simml.
F; 1566/Domain: protein-tyrosine-phosphatase homology simml.
F; 1664-1887/Domain: protein-tyrosine-phosphatase homology simml.
F; 164-1887/Domain: protein-tyrosine-phosphatase homology simmly simmly site: cys (phosphocysteine intermediate) #status predicted
F; 1839/Active site: Cys (phosphocysteine intermediate) #status predicted
F; 1845/Bainding site: substrate phosphate (Arg) #status predicted
F; 1845/Bainding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                       1433 CSAGVGRIGVFITLSIVLERMRYEGVVDIFQTVKVLRTQRPAMVQTEDBYQFCFQAALEY
                                                                                                                                                                                                                                               VRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSH----ITGPLLVH
                                                                                                                                                                                                                                                                                                                                                                             172 CSAGVGRIGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEV
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41.1%; Pred. No. 1e-35;
tive 46; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Overy Match
Best Local Similarity 41.1.
Best Local Similarity 61.1.
Conservative
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                                          1258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein-tyrosine-phosphatase (EC 3.1.3.48) 2B, splice form LAR - rat
District and the corrections of the common antigen-related phosphatase
(Species: Rattus norvegicus (Norway rat)
(Species: Rattus norvegicus (Norway rat)
(Species: Rattus norvegicus (Norway rat)
(Species: Rattus norvegicus (Norway rat)
(Species: Rattus norvegicus (Norway rat)
(Species: Rattus norvegicus (Norway rat)
(Species: 159148) 54618
(Rattus norvegicus (Norway rat)
(Species: 159148) 54618
(Rattus norvegicus (Norvegicus type protein tyrosine phosphatase is expressed during neurogen Apacession: 158148) MUD: 93357030; PMID: 8352946
(Apacession: 158148) MUD: 934778PHOS, release 113.0, the source is designated as Rattus in Genbank entry RATTYRPHOS, release 113.0, the source is designated as Rattus in Genbank entry RATTYRPHOS, release 113.0, the source is designated as Rattus in Genbank entry RATTYRPHOS, release 113.0, the source is designated as Rattus in Genbank entry RATTYRPHOS, release 113.0, the source is designated as Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus predicted and related procein; phosphatese homology capp.

Flat A. Residues in Amandogolobulin homology capp.

Flat A. Robert in Rattus protein-tyrosine-phosphatese homology capp.

Flat A. Robert in Rattus protein-tyrosine-phosphatese homology capp.

Flat A. Robert in Rattus predicted represented intermediate) Hink PTP1 Hatatus predicted Flat Rattus predicted Flat Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus in Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAGVGRIGVFICVDVVFSAIBKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYBIVLEVL 232
                                                                                                                                                                                                                                                                                                                                                                                 1 QNRDKNRYRDILPYDSTRVPLG----KNKDYINASYIRIVNHEEEYFYIATQGPLPETIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKY----VR-YVRKSHITGPLLVHC
                                                                                                                                         Gaps
                                                                                                                                         12;
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                                                                      Length 1337;
F;1245/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                     Indels
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                                                                                                                                         83;
                                                                  ; DB 1;
6.1e-36;
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                                                                                                                                     48; Mismatches
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; Pred. No. 7.9e
46; Mismatches
                                                                  37.9%; Score 475; 40.7%; Pred. No. 6
                                                                                                  Local Similarity 40.7 es 98; Conservative
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Best Local Similarity
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                                                                      Query Match
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9

Gaps

15;

98

1779 LREFKVTDARDGOSRTVROFOFTDWPEQGAPKSGEGFIDFIGQVHKTKEQFGQDGPISVH 1838

P

26

2 NRDKNRYRDILPYDSTRVPLG-----KNKDYINASYIRIVNHEEEYFYIATQGPLPETIE

Matches

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Cytacesion: 150212
R;Stoker, A.W.
Mech. Dev. 46, 201-217, 1994
A;Title: Isoforms of a novel cell adhesion molecule-like protein tyrosine phosphatase ar
A;Reference number: 150212; MUID:95001563; PMID:7918104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:090815; GB:L32780; NID:9485746; PIDN:AAA64460.1; PID:9485747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.7.Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase F.148-208/Domain: immunoglobulin homology <IMM1>
F.245-299/Domain: immunoglobulin homology <IMM2>
F.245-299/Domain: immunoglobulin homology <IMM2>
F.317-399/Domain: fibronectin type III repeat homology <3FR>
F.311-499/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F.1257-1479/Domain: protein-tyrosine-phosphatase homology <FFP2>
F.1147/Active site: Cys (phosphocyteine intermediate) #status predicted
F.1147/Binding site: substrate phosphate (Arg) #status predicted
F.1438/Active site: Cys (phosphocyteine intermediate) #status predicted
F.1438/Binding site: substrate phosphate (Arg) #status predicted
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DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVF-LETFHVTQYFT 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Species: Gallus gallus (chicken)
C.Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 NRDKNRYRDILPYDSTRVPLG-----KNKDYINASYIRIVNHEEEYFYIATQGPLPETIE
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                                                   116 VRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSH----ITGPLLVH
                                                                                                                                                                                                                                                                                                     172 CSAGVGRIGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEV
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; Pred. No. 1.7e-35;
46; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-tyrosine-phosphatase (EC 3.1.3.48) - chicken
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A;Molecule type: mRNA
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Best Local Similarity 41.1
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Cancer Res. 52, 737-740, 1992
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A; Residues: 1-1912 <PUL.
A; Cross-references: UNIPROT: P23468; GB:L38929; NID:g755652; PIDN: AAC41749.1; PID:g755653
R; Krueger, N.X.; Streuli, M.; Saito, H.
EMBO J. 9, 3241-3252, 1990
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C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
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A,Reference number: S12049; MUID:91006018; PMID:2170109
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1200-309/Domain: immunoglobulin homology <IMM3>
1210-3109/Domain: immunoglobulin homology <IMM3>
1211-811/Domain: immunoglobulin homology <IMM3>
1211-811/Domain: immunoglobulin homology <IMM3>
1213-1912/Domain: leukocyte common antigen cytosolic domain homology <IAC>
1669-1892/Domain: protein-tyrosine-phosphatase homology <PTP2>
15133/Active site: Cys (phosphocyteine intermediate) #status predicted ils59/Binding site: substrate phosphate (Arg) #status predicted il884/Active site: Cys (phosphocysteine intermediate) #status predicted
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A;Cross-references: GB:S78086; NID:g243545; PIDN:AAB21147.1; PID:g243546
A;Cross-references: GP:S78086; NID:g243545; PIDN:AAB21147.1; PID:g243546
A;Csperimental source: pre-B cell NALM-6
A;Note: sequence extracted from NOBI backbone (NCBIN:78086, NCBIP:78087)
A;Note: the authors did not report the entire codon for residue 90
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A;Accession: A56178
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Mismatches 82
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A,Accession: S51174
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A,Cross-references: EMBL:111587; NID:g205134; PIDN:AAC37656.1; PID:g205135
A,Cross-references: EMBL:111587; NID:g205134; PIDN:AAC37656.1; PID:g205135
B,Yan, H.; Grossman, A.; Wang, H.; D'Eustachio, P.; Mossie, K.; Musacchio, J.M.; Silvenr.
A,Raio. Chem. 268, 24880-24886, 1993
A,Title: A novel receptor tyrosine phosphatase-sigma that is highly expressed in the nex A,Reference number: A49104; MUID:94043351; PMID:8227050
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F;1-26/Domain: signal sequence #status predicted <51G>
F;27-1863/Product: protein-tyrosine-phosphatase #status predicted <MAT>
F;149-209/Domain: immunoglobulin homology <1MM1>
F;246-300/Domain: immunoglobulin homology <1MM2>
F;318-400/Domain: fibronectin type III repeat homology <FN3B>
F;318-400/Domain: fibronectin type III repeat homology <FN3B>
F;314-499/Domain: fibronectin type III repeat homology <FN3C>
F;314-1863/Domain: fibronectin type III repeat homology <FN3C>
FN3C-1863/Domain: fibronectin type III repeat homology <FN3C>
FN3C-1863/Domain: fibronectin type III repeat 
                                                                                                                        receptor-like protein-tyrosine-phc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C, Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1620 NKFKNRLVNILPYESSRVCLQPIRGVEGSDYINASFID--GYRQQKAYIATQGPLAETTE 1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 VRVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSH----ITGPLLVH 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---KNKDYINASYIRIVNHEEEYFYIATQGPLPETIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVF-LETFHVTQYFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Status: preliminary, not compared with conceptual translation
R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, Biochem. J. 302, 39-47, 1994
A;Title: Molecular cloning and expression of a unique receptor A;Reference number: S46216; MUID:94347119; PMID:8068021.
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: nucleic acid
A;Residues: 1-596,'R',598-603,'I',967-1788,'G',1790-1863 <YAN>
A;Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: sequence extracted from NCBI backbone (NCBIP:139669)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 37.4%; Score 468.5; DB 2; Best Local Similarity 40.7%; Pred. No. 3.7e-35; Matches 98; Conservative 46; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q64605; EMBL:L11587
R;Goldstein, B.J.
submitted to the EMBL Data Library, February 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1, 2004, 12:17:27
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                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-1863 <ZHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L 1855
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                                               procession states (EC 3.1.3.48), receptor type beta precursor - human c)Species: Homo sapiens (man) C;Species: 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: S12050; S18818; S18439 R;Krueger, N. X; Streull, M.; Saito, H. EMBO U. 9, 3241-3222, 1990 A;Title: Structural diversity and evolution of human receptor-like protein tyrosine phos A;Reference number: S12049; MUID:91066018; PMID:2170109 A;Reference number: S12049; MUID:91066018; PMID:2170109 A;Reference number: S12049; MUID:91066018; PMID:2170109 A;Reference number: S12049; MUID:91066018; PMID:2170109 A;Reference number: S12049; MUID:9104011; NID:935787; PIDN:CAA38066.1; PID:935788 A;Reternce number: S12818 MUID:91243813; PMID:1645282 A;Title: Expression of a truncated protein-tyrosine phosphatase mRNA in human lung. A;Reference number: S15818 MUID:91243813; PMID:1645282 A;Accession: S15818 A;Accession: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reternce number: S15818 A;Reter
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A,Map position: 12q15-12q21

A,Map position: 12q15-12q21

A,Map position: 12q15-12q21

C,Superfamally: protein-tyrosine-phosphatase, receptor type beta; fibronectin type III re C,Superfamally: protein-tyrosine-phosphatase, receptor alternative splicing; phosphoprotein; phosphoric monoester hydrolase; receptor E,1-22/Domain: signal sequence #status predicted <SIG>
E,3-1525/Domain: extracellular #status predicted <ETT>
F,1626-1642/Domain: transmembrane #status predicted <ETM>
F,1626-1642/Domain: intracellular #status predicted <ETM>
F,1627-1952/Domain: protein-tyrosine-phosphatase homology <PTP>
F,1927-1952/Domain: protein-tyrosine-phosphatase homology <PTP>
F,1910/Active site: Cys (phosphocysteine intermediate) #status predicted
F,1910/Binding site: substrate phosphate (Arg) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ONRDKNRYRDILPYDSTRVPLGK-----NKDYINASYIRIVNHEEEYFYIATQGPLPETI
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Pred. No. 3.2e-35;
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1 QNRDKNRYRDILPYDSTRVP......MIQTKEQYQFCYEIVLEVLQ 233
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| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1582122 seqs, 356623098 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
                                                                                                                                                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Semient & sample	, a	Semience 1, Applia	Semience 2 Applia	, u	Semience 3, Appril		י ר		, ,	000	Sequence 56, Appl	12		į
SUMMARIES		QI	US-09-095-478-6	US-09-095-478-8	US-09-095-478-1	US-09-095-478-2	US-09-095-478-3	US-10-311-764-4	US-09-095-478-4	US-09-095-478-7	US-09-095-478-9	TIS-10-060-018-35	UU 100 000 01 011	94-585-60-01-60	US-10-177-980-12	US-10-795-148-2	
		DB	10	10	10	10	10	15	10	10	10	14	, ,	1	14	17	
		Match Length DB	354	379	426	463	412	420	122	381	358	1267	1267	071	2466	2466	
٥¥	Query	Match	100.0	100.0	100.0	100.0	93.7	80.0	53.3	47.8	47.3	47.3	47.3		47.3	47.3	
		Score	1253	1253	1253	1253	1174	1003	668	598.5	592.5	592.5	592.5	1 0	535.5	592.5	
	Result	No.	ч	2	٣	4	S	9	7	8	6	10	11		77	13	

Sections 46 Appl	4 4	134	equence 5.	6	σ	9.4	equence 9	· u	΄ ς	1 4	(1)	, '.		Sequence 55. Appl	Sequence 45. Appl	4	΄ ζ	equence 54	Sequence 4	9	m	7	4	4	2	equence 167	equence 6	emience 7.	. 4	equence 54.	equence 2	
US-09-802-669-46	S-10-619-22	-10-408-	9-09	t	0 - 218 - 779	0	8-779	072-012-8		-10 - 293	US-10-366-547-38	-294-	5-10-293-23	US-09-808-602-55	-09-800-19	96-5	US-09-788-626-22	Ŋ		US-10-245-539-6		US-10-390-501-2	37 14 US-10-366-547-42	US-10-366-547-44	US-10-723-606-2	US-10-408-765A-1670	US-10-634-027-6	US-10-634-027-7	US-10-634-027-4	US-09-909-567B-54	US-10-634-027-2	
6	15	16	10	15	15	15	15	15	σ	14	14	6	14	σ	10	14	σ	σ	10	14	16	14	14	14	16	16	15	15	15	10	15	
2485	2485	2485	122	263	263	235	235	235	913	913	913	244	244	1948	1948	703	291	ß	1502	264	341	1337	1337	1337	1337	344	312	319	336	6	1997	
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14	15	16	11	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	6E	40	41	42	43	44	45	

ALIGNMENTS

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RESULT 1

US-09-095-478-6

US-09-095-478-6

Sequence 6, Application US/09095478

Publication No. US20030095970A1

SEQUENCE 6, Application NOVEL PROTEIN TYROSINE
TITLE OF INVENTION:
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION DATA:
ADDITOTION NUMBER: US/09/095,478
FILING DATE:
TILING DATE:
TILING DATE:
TILING DATE:
TILING DATE:
TILING DATE:
TILING DATE:
TILING DATE:
TILING DATE:
THERRY APPLICATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/115
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Gaps

. 0

Indels

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61 MYLENNCAVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                               121 IVKKSTGKSÇÇVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTG 180
                                                                                                                                                                                                                                                                                             263 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRVVRKSHITGPLLVHCSAGVGRTG 322
                                                                                                                                                                                                                                                                  1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 VFICVDVVFSAIBKNYSFDIMNIVTOMRKORGRAIQTKBOYOFCYBIVLEVLQ 233
                                                                                                                                                                                      h Similarity 100.0%; Score 1253; DB 10; Length 379; Similarity 100.0%; Pred. No. 1.6e-125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09095478

Publication No. US20030095970A1

GENERAL INFORMATION:
APPLICANT: Blowman, Gregory
ITILE OF INVENTION: PHOSPHATASE SUPTPOS AND
ITILE OF INVENTION: PHOSPHATASE SUPTPOS AND
ITILE OF INVENTION: METATED PRODUCTS AND
ITILE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 224,1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32,327
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                    LENGTH: 379 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 233; Conservative
                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                  MOLECULE TYPE: Peptide US-09-095-478-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                       linear
67-3510
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                                                                                                                         TOPOLOGY:
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CITY: Lo
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US-09-095-478-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 VFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 VFICVDVVFSAIERNYSFDIMNIVTQMRKQRCGMIQIKEQYQFCYEIVLEVLQ 350
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0
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                                                                                                                                                                                                                                                                          100.0%; Score 1253; DB 10;
100.0%; Pred. No. 1.4e-125;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plowman, Gregory
VENTION: NOVEL PROTEIN TYROSINE
NOVEL PHOSPHATASE SUPTPO5 AND
VENTION: RELATED PRODUCTS AND
VENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: TBM Compatible
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 224/115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327
                               TELEPAN: (213) 489-1600
TELEPAN: (213) 955-0440
TELERA: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 354 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOV TITLE OF INVENTION: PHO TITLE OF INVENTION: REL. TITLE OF INVENTION: MET NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS: ADDRESSEE: LYON & LYON ADDRESSEE: LYON & LYON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                    233; Conservative
                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 233; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
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Gaps

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225 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ 284
                                                                                                                                                                                                                                                                       61 MVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQ 120
                                                                                                                                                                                                                                                                                               285 MVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQ 344
                                                                                                                                                                                                                                                                                                                                                          121 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTG 180
                                                                                                                                                                                                                                                                                                                                                                                              345 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTG
                                                                                                                                                                                 1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 VFICVDVVFSALEKNYSFDIMNIVTOMRKORGGMIQTKEQYQFCYBIVLEVLQ 233
                                                                                                DB 10; Length 463;
                                                                                                                                           Indels
                                                                                                                                         .
                                                                                              100.0%; Score 1253; DB 1(100.0%; Pred. No. 2e-125; Live 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
ITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: Storage COMPUTER: 1EM Compatible OPERATING SYSTEM: 1EM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478 FILING DATE:
CLASSIFFCATION:
RICHARD APPLICATION DATA:
APPLICATION DATA:
RICHARD DATE:
RILING DATE:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNET, PREME ATTORNOON TO REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 412 amino acids TYPE: amino acid
                                                                                                                    Best Local Similarity 100.
Matches 233; Conservative
                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
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STATE: California
COUNTRY: U.S.A.
        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE:
US-09-095-478-3
           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                   US-09-095-478-2
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                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                             61 MVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                121 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTG 180
                                                                                                                                                                                                                                                                                                                                                        308 IVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTG 367
                                                                                                                                                                                                                                         1 QNRDKONRYRDILPYDSTRVPLGKOKDYINASYIRIVNHEBEYFYIATQGPLPETIEDFWQ 60
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 VFICVDVVFSALEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
0
                                                                                                                                                    100.0%; Score 1253; DB 10; Length 426; 100.0%; Pred. No. 1.8e-125;
                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09095478
Publication No. US20030095970A1
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPPOS AND
TITLE OF INVENTION: PHOSPHATASE SUPPOS AND
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE:
SARRET: 633 West Fifth Street
STREET: Said West Fifth Street
                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPOTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastESQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WATDING, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 224
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: _linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 233; Conservative
                                                              TOPOLOGY: linear in MOLECULE TYPE: Peptide US-09-095-478-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-095-478-2
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                                                                                                                                                                                                                                                                                                                                                                      188 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEERYFYIATGGPLPETIEDFWQ 247
                                                                                                       1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEFYFYIATQGPLPETIEDFWQ
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  Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENDERAL INFORMETION:
APPLICANT: INCYTE GENOMICS, INC.; AU-YOUNG, Janice K.
APPLICANT: BAUGHW, Mariah R.; DING, Li
APPLICANT: BAUGHW, Mariah R.; DING, Li
APPLICANT: ELLIOTT, Vicki S.; GANDH, Ameena R.
APPLICANT: KERAREY, Liam; LEE, ETTERLIA, April J.A.
APPLICANT: KERAREY, Liam; LEE, ETTERLIA, Madhusudan M.
APPLICANT: AVIZU, Chandra S.; RAMKUMALA, Madhusudan M.; SANJANWALA, Madhusudan M.; SANJANWALA, Madhusudan M.; APPLICANT: REDDY, Roopa M.; SANJANWALA, Madhusudan M.; APPLICANT: REDDY, Roopa M.; SANJANWALA, Madhusudan M.; APPLICANT: THORNITON, Michael B.; TRIBOULEY, Catherine M.; APPLICANT: CHAWLA, Narinder K.; YUE, Henry
APPLICANT: CHAWLA, Narinder K.; YUE, Henry
TITIE OF INVENTION: PROFIEND PHOSPHATASES
FILE REPERENCE: PL-0126 USN
CURRENT FILING DATE: 2001-06-14
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/212,447
PRIOR APPLICATION NUMBER: US 60/212,447
PRIOR APPLICATION NUMBER: US 60/215,210
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/215,210
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/215,210
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
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OTHER INFORMATION: Incyte ID No. US20040023245A1 7476861CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25; Indels
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 VFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 405
                                                                                                                                                                                                                                                                                                                                                                                                                                              VFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTK 218
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80.0%; Score 1003; DB 15;
Best Local Similarity 78.9%; Pred. No. 1.2e-98;
Matches 183; Conservative 24; Mismatches 25;
93.7%; Score 1174; DB 10;
100.0%; Pred. No. 5.2e-117;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10311764 Publication No. US20040023245A1 GENERAL INFORMATION:
                                                               218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
           Query Match
Best Local Similarity
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243 VLENNSNVIAMITREIBGGIIKCYHYWPISLKKPLELKHFRVFLEDNYQILQYFIIRMFQV 302
                                                                                                                                                                        122 VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 DFWQMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTV
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                                                               VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI
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                                                                                                                                                                                                                                                           363 PLCVDVVFCAIVKNCSFNIMDIVAQMREQRSGMVQTKEQYHFCYDIVLEVLR 414
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                                                                                                                                                                                                                                     182 FICYDVVFSAJEKNYSFDIMNIVTOMRKORCGMIQTKEQYQFCYEIVLEVLQ
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53.3%; Score 668; DB 10; Length 122;
Best Local Similarity 100.0%; Pred. No. 2e-63;
Matches 122; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-09-095-478-4
is-09-095-478-4
; Sequence 4, Application US/09095478
; Publication No. US20030095970A1
; GENERAL INFORMATION:
APPLICANT: Plowman, Gregory
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPTPOS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 90071-2000
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FRSESSO FOR Windows 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FASTSEQ for Windows 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/095,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 224/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PHO
TITLE OF INVENTION: PHO
TITLE OF INVENTION: RELITITLE OF INVENTION: MET
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS: 3
ADDRESSEE: LYON & LYON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: Peptide US-09-095-478-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
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ZIP: 90071-2066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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241 TLEDIQTREVRHISHLNFTAWPDHDTPSQPDDLLTFISYMRHIHRSGPITTHCSAGIGRS 300
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                    177 GRIGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVL 232
                                           180 GVFICVDVVFSAIBKNYSFDIMNIVTQMRKQRCGMIQTKEQVQFCYEIVLEVL 232
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                                                                                                                                                                                                            APPLICANT: PLOWMAN, Gregory
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE SUPTPOS AND
TITLE OF INVENTION: RELATED PRODUCTS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSES: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FASTSEQ for Windows 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/095,478
                                                                                                                                                    ; Sequence 9, Application US/09095478; Publication No. US20030095970A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : (213) 489-1600
(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 amino acids
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MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                  Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid STRANDEDNESS: six
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90071-2066
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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TELEX: 6'
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                                                                                                                                      JS-09-095-478-9
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CITY: L
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                  61 RVFQIVKKSTGKSQCVKHLQPTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGV 120
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RVFQIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 MVLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFTVRVF 119
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50.0%; Pred. No. 2.6e-55;
Mismatches 74; Indels
                                                                                                                                                                                                                                                                        Plowman, Gregory
TENTION: NOVEL PROTEIN TYRCSINE
VENTION: PHOSPHATASE SUPTPOS AND
VENTION: RELATED PRODUCTS AND
VENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTY U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastESG for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,478
                                                                                                                                                                                                                                                                                                                                                                                                              E: Lyon & Lyon
633 West Fifth Street
Suite 4700
                                                                                                                                                                                                            Sequence 7, Application US/09095478; Publication No. US20030095970A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFRENCE/DOCKET NUMBER: 224/
TELECOMMUNICATION INFORMATION:
TELEPAK: (213) 489-1600
IELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
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LENGTH: 381 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 118; Conservative
                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Plowman, Greg
TITLE OF INVENTION: NOVE
TITLE OF INVENTION: PHOS
TITLE OF INVENTION: RELA
TITLE OF INVENTION: RELA
TITLE OF INVENTION: METH
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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California
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Best Local Similarity
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                                                                          GR 178
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                                                                                                                                                                       RESULT 8
US-09-095-478-7
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STREET:
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Ota, Toshio
GENERAL INFORMATION:
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US-10-177-980-12
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                                                                                                      APPLICANT:
APPLICANT:
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TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-099002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ONRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ
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    301 GTLICIDVVLGLISQDLDFDISDLVRCMRLQRHGMVQTEDQYIFCYQVILYVL 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR PELICATION NUMBER: US 60/159,590
PRIOR PILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 1999-07-29
PRIOR PLING DATE: 1999-07-29
PRIOR PELICATION NUMBER: UP 11-248036
PRIOR PILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: UP 2000-118776
PRIOR APPLICATION NUMBER: UP 2000-183767
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-06-09
PRIOR PILING DATE: 2000-06-09
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                                                                                                          Sequence 35, Application US/10060065
Publication No. US20030017480A1
                                                                                                                                                                                                                                                                                                                                                                                 Tetsuji Otšuki
Shin-Ichi Funahashi
                                                                                                                                                                                                                                                          Kaoru Otsuka
Jun-Ichi Yamamoto
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                                                                                                                                                                                                                Tetsuo Nishikawa
                                                                                                                                                                                                                                                                                                                                                                Keiichi Nagai
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                                                                                                                                                                                                                                                                                                                                                                                                                             Chiaki Senoo
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APPLICANT: Takao Isogai
                                                                                                                                                                                                                                           Koji Hayashi
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US-10-060-065-35
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LENGTH: 1267
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APPLICANT:
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APPLICANT:
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APPLICANT:
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US-10-059-585-56; Sequence 56, Application US/10059585; Publication No. US20030082776A1

RESULT 11

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APPLICANT: Saras, Jan
APPLICANT: Franzi, Petra
APPLICANT: Pranzi, Petra
APPLICANT: Hellman, Ulf
APPLICANT: Hellman, Ulf
APPLICANT: Gones, Leonel Jorge
APPLICANT: Gones, Leonel Jorge
APPLICANT: Heldin, Carl-Henrik
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PIPLI
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CURRENT FILING DATE: 2002-01-29
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%; Pred. No. 5.4e
41; Mismatches
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PRIOR APPLICATION NUMBER: PCT/JP00/05060
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-17
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
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                                               Hayashi, Koji
Otsuka, Kaoru
Yamamoto, Jun-ichi
Ishii, Shizuko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.3%;
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Isogai, Takao
Nishikawa, Tetsuo
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Best Local Similarity 47.6'
Matches 111; Conservative
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US-10-059-585-56
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47.38;
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Best Local Similarity
Matches 111; Conservat
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US-10-619-220-46
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US-09-802-669-46
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                                                                                                                                                                                                                                                                                        Query Match
47.3%; Score 592.5; DB 14; Length 2466;
Best Local Similarity 47.6%; Pred. No. 1.3e-53;
Matches 111; Conservative 41; Mismatches 80; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10795148
; Publication No. US20040224337A1
; Publication No. US20040224337A1
; APPLICANT: FOEH, ERIK
; APPLICANT: JORENTE, GUSTAVO A.
; APPLICANT: USFER, ENAN
; TITLE OF INVENTION: USE OF BIOMOLECULAR TARGETS IN THE
; TITLE OF INVENTION: USE OF BIOMOLECULAR TARGETS IN THE
; TITLE OF INVENTION: USE OF SOME AND VISUALIZATION OF TUMORS
; FILE REFERENCE: AGYT-022
; CURRENT APPLICATION NUMBER: US/10/795,148
; CURRENT FILING DATE: 2004-03-04
; PRIOR FILING DATE: 2003-03-04
            CURRENT APPLICATION NUMBER: US/10/177,980
CURRENT FILING DATE: 2002-06-21
PRIOR PELLING DATE: 1998-05-18
PRIOR FILING DATE: 1998-05-18
PRIOR FILING DATE: 1997-02-25
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
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Conservative 41;
FILE REFERENCE: L0461/7030
                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 111; Conserv
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US-10-795-148-2
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US-10-177-980-12
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US-10-795-148-2
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Sequence 46, Application US/09802669;
Patent No. US20020004490A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Marcusson, Eric G.
APPLICANT: Watt, Jacqueline
APPLICANT: Marcusson, Eric G.
APPLICANT: Marcusson, Eric G.
APPLICANT: Application and Antisense Compound Modulation of Fas Mediated Signaling
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
TITLE REPRENENCE: ISPH-545
CURRENT APPLICATION NUMBER: US/09/802,669
CURRENT APPLICATION NUMBER: US 09/665,615
PRIOR APPLICATION NUMBER: US 09/65,615
PRIOR APPLICATION NUMBER: US 09/65,615
PRIOR APPLICATION NUMBER: US 09/65,615
SPRIOR PILING DATE: 1999-04-12
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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| Publication No. US20040033979A1
| GENERAL INFORMATION:
| APPLICANT: Dean, Nicholas M.
| APPLICANT: Marcusson, Eric G.
| APPLICANT: Marcusson, Eric G.
| APPLICANT: Marcusson, Eric G.
| APPLICANT: Marcusson, Eric G.
| APPLICANT: Marcusson, Eric G.
| APPLICANT: Marcusson, Eric G.
| APPLICANT: Marcusson, Eric G.
| APPLICANT: Marcusson, Eric G.
| APPLICANT: Manage, Hong
| TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
| TITLE OF INVENTION: ADMISE: US/10/619,220
| CURRENT APPLICATION NUMBER: US/10/65,665
| PRIOR FILING DATE: 2001-03-01
| PRIOR FILING DATE: 2000-09-18
| PRIOR APPLICATION NUMBER: US 09/655,615
| PRIOR FILING DATE: 1999-04-12
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Pred. No. 1.3e-53;
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1; Gaps
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Best Local Similarity 47.3%; Score 592.5; DB 15; Length 2485;
Best Local Similarity 47.6%; Pred. No. 1.3e-53;
Matches 111; Conservative 41; Mismatches 80; Indels 1;
                                                                                                                                                                                                                                                                                                 Search completed: December 1, 2004, 12:52:37 Job time: 425.441 secs
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 2485
; TYPE: PRT
; ORGANISM: Homo sapiens
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Query Match
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612.993 Million cell updates/sec
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2: /cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptcdata/1/iaa/pcTUS_COMB.pep:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-290-640-46

US-09-848-294-2

US-09-848-294-7

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US-09-848-294-7

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US-09-848-294-2

US-09-844-295-21

US-09-158-65-5

US-09-158-65-5

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APPLICANT: GONEZ, LEONEL JORGE
APPLICANT: SARAS, JAN
APPLICANT: SARAS, JAN
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: HELDIN, CREH-HENRIK
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TITLE OF INVENTION: TXROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ALLANTIC AVENUE
CITY: BOSTON
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MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPPRATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 09-AUG-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.3%; Score 592.5; DB 2; 47.6%; Pred. No. 1.2e-60;
                                                                                     US-08-087-244A-2
US-08-743-492A-9
US-09-743-492A-9
US-08-449-644-8
US-08-087-244A-8
US-08-948-294-9
US-08-91-254A-9
US-08-652-971-4
US-08-991-258A-4
US-08-991-953A-4
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US-08-144-955-26
US-08-144-992-26
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APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08596291
Patent No. 5821075
GENERAL INFORMATION:
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TELECOMUNICATION INFORMATION
TELEPHONE: 617/720-3500
TELEPAX: 617/720-2441
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TELEX: 92-1742 EZEKIEL
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2465 amino acids
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TOPOLOGY: linear
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GENERAL INFORMATION:

APPLICANT: Saras, Jan

APPLICANT: Franzn, Petra

APPLICANT: Franzn, Petra

APPLICANT: Hellman, Ulf

APPLICANT: Hellman, Ulf

APPLICANT: Hellman, Ulf

APPLICANT: Hellman, Ulf

APPLICANT: Hellman, Ulf

APPLICANT: Hellman, Ulf

APPLICANT: Hellman, Ulf

APPLICANT: Hellman, Ulf

APPLICANT: Hellman, Ulf

APPLICANT: Hellman, Ulf

APPLICANT: Hellman, Ulf

CURENT: Hellin, Carl Henrik

TILLB OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPLI

FILE REFERENCE: L0461/7030

CURRENT APPLICATION NUMBER: 08/805,583

CURRENT FILING DATE: 1997-02-25

NUMBER: OF SEQ ID NOS: 39

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 MYLENNCNVIAMITREIECGVIKCYSYWPISL-KEPLEFEHFSVFLETFHVTQYFTVRVF 119
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                                                                                                                                                                                                                  120 QIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRT 179
                                                                                                                                                                    2276 MIWEQKSTVIAMMIQEVBGEKIKCQRYWPNILGKTIMVSNRLRLALVRWQQLKGFVVRAM
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                                                        1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ
                    Gaps
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                    Indels
Pred. No. 1.2e-60;
1; Mismatches 80;
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47.6%; Pred. No. 1.2e-60;
cive 41; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-080-855-12; Sequence 12, Application US/09080855A; Patent No. 6083721
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  Best Local Similarity 47.6%; Pr
Matches 111; Conservative 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 111; Conservative
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Best Local Similarity
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TYPE: PRT
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                                                                                                                                                                                                      120 QIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRT 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIMARY STRUCTURE AND FUNCTIONAL
EXPRESSION OF NUCLECTIDE SEQUENCES FOR NOVEL PROTEIN
TYROSINE PHOSPHATASES
                                         1 ONRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ
                                                                                                                                                                                                                                                                                                            GVFICVDVVFSAIEKNYSFDIMNIVTOMRKORCGMIQTKEQYOFCYEIVLEVL 232
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      Indels
        80;
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      41; Mismatches
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CLASSIFICATION:
PRIOR PAPELICATION:
PRIOR PAPELICATION DATA:
APPLICATION NUMBER: US 08/596,291
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 01-SEP-1994
ATTOCNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GREENFIELD & SACKS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02210
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: ISM PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,804
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09100804
Patent No. 6066472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SARAS, JAN
CLAESSON-WELSH, LENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GONEZ, LEONEL JORGE
APPLICANT: SARAS, JAN
APPLICANT: CLAESSON-WELSH, LENP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: PREMARY ST
TITLE OF INVENTION: EXPERSION
TITLE OF INVENTION: TYROSINE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 31,616
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 2465 amino acids
amino acid
      Conservative
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USA
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6066472
GENERAL INFORMATION:
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STATE: MASSAC
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        111;
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US-09-100-804-3
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TELECOMMUNICATION INFORMATION
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US-09-290-640-46
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       APPLICANT: Aspenstrm, Pontus
APPLICANT: Hellman, UIC
APPLICANT: Hellman, UIC
APPLICANT: Heldin, Carl-Henrik
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PTPL1
FILLE REPERENCE: L0461/7030
CURRENT APPLICATION NUMBER: US/09/566,076
CURRENT APPLICATION NUMBER: 09/080,855
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2277 MIWEOKSTVIAMMTQEVEGEKÍKCORÝWPNILGKTTMVSNRLRLALVRMQQLKGFVVRAM 2336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 QIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRT 179
                                                                                                                                                                                                                                                                                                                                                                                                                   1 ONRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 GVFICVDVVFSAIEKNYSPDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVL 232
                                                                                                                                                                                                                                                                                                                                         47.3%; Score 592.5; DB 4; Length 2466; 47.6%; Pred. No. 1.2e-60;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
                                                                                                                                                                                                                                                                                                                                                                               41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: TWOMEY, MICHAEL J.
REGISTRATION NUMBER: P-38,349
REFERENCE/DOCKET NUMBER: L0461/7000WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: PCT/US94/09943
01-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application PC/TUS9409943
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
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STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 47.69
Matches 111; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT:
TITLE OF INVENTION: P
TITLE OF INVENTION: T
TITLE OF INVENTION: T
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 03 CLASSIFICATION:
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PCT-US94-09943-2
                                                                                                                                                                                                                                                       LENGTH: 2466
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Sequence 46, Application US/09290640

Patent No. 6204055

GENERAL INFORMATION:
APPLICANT: Barcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling FILE REPERENCE: ISPH-0351

CURRENT APPLICATION NUMBER: US/09/290,640

CURRENT FILING DATE: 1999-04-12

NUMBER OF SEQ ID NOS: 85

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 46

LENGTH: 2485
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                                                                                                                                                                                                                                 47.3%; Score 592.5; DB 5;
47.6%; Pred. No. 1.2e-60;
live 41; Mismatches 80;
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TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
TELEX: 92-1742 EZEKIEL
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENTH: 2466 amino acids
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 47.69
Matches 111; Conservative
                                                                                                                                                                       MOLECULE TYPE: protein
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Gaps

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WS-09-848-294-7

WS-09-848-294-7

Sequence 7, Application US/09848294

Patent No. 64796404

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas K.

TITLE OF INVENTION: 1502/ation of A cDNA Encoding A No. 6479640el

TITLE OF INVENTION: Protein Tyrosine Phosphotase Which Localizes to Focal

TITLE OF INVENTION: Adhesions and Uses Therefor

TITLE OF INVENTION: Adhesions and Uses Therefor

TITLE OF INVENTION: Adhesions and Uses Therefor

TITLE OF INVENTION: Adhesions and Uses Therefor

CURRENT APPLICATION NUMBER: US/09/848,294

CURRENT FILING DATE: 1999-01-22

PRIOR FILING DATE: 1999-01-22

PRIOR FILING DATE: 1999-01-22

PRIOR FILING DATE: 1999-01-23

PRIOR APPLICATION NUMBER: 08/107,420

PRIOR APPLICATION NUMBER: 07/663,579

PRIOR APPLICATION NUMBER: 07/663,579

PRIOR APPLICATION NUMBER: 07/494,036

PRIOR FILING DATE: 1999-03-14
                                                                                                                                                                                                              724 TCAQFWQVVWDQKLSLIVMLTTLTERGRTKCHQYWP---DPPDVMNHGGFHIQCQSEDCT 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 HCSAGVGRIGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLE 230
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al Similarity 42.0%; Pred. No. 3.7e
102; Conservative 38; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-848-294-7
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        Query Match
Best Local {
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j Sequence 2, Application US/09848294

patent No. 6479640

GENERAL INFORMATION:

APPLICANT: Tonks, Nicholas K.

TITLE OF INVENTION:

TITLE OF INVENTION: Protein Tyrosine Phosphotase Which Localizes to Focal

TITLE OF INVENTION: Adhesions and Uses Therefor

TITLE OF INVENTION: Adhesions and Uses Therefor

FILE OF INVENTION: Adhesions and Uses Therefor

FILE OF INVENTION: Adhesions and Uses Therefor

FILE OF INVENTION: Adhesions and Uses Therefor

FILE OF INVENTION: Adhesions and Uses Therefor

FILE OF INVENTION: Adhesions and Uses Therefor

FRICR REPERROR: CSH190-04FZA

CURRENT FILING DATE: 1999-01-22

PRIOR APPLICATION NUMBER: 08/159,536

PRIOR FILING DATE: 1996-12-04

PRIOR PLING DATE: 1991-03-04-6

PRIOR PLING DATE: 1991-03-14

PRIOR APPLICATION NUMBER: 07/663,579

PRIOR APPLICATION NUMBER: 07/663,579

PRIOR FILING DATE: 1991-03-14

NUMBER OF SEQ ID NOS: 13

CSOTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 913

TAVER: DOWN 100-1
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                                                    Sequence 46, Application US/09665615B
Sequence 46, Application US/09665615B
Sequence 46, Application US/09665615B
Sequence 46, Application US/09665615B
Sequence 46, Application US/09665615B
Sequence 46, Application US/09665615B
APPLICANT: Warch Sequence 6, APPLICANT: Warch Artisense Modulation of Fas Mediated Signaling
TILE OF INVENTION: Antisense Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0502
CURRENT APPLICATION NUMBER: US/09/665,615B
CURRENT FILING DATE: 2000-09-18
PRIOR PILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 179
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: PatentIn Ver. 2.0
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47.6%; Pred. No. 1.2e-60;
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Matches 111; Conservative
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US-09-848-294-2
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                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 CSAGIGRIGVLVIMETAMCLTERNLPIYPLDIVRKMRDQRAMMVQTSSQYKFVCEAILRV 232
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                                                                                                                                                                                                                                   APPLICANT: Ullrich, Axel
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE
TITLE OF INVENTION: PHOSPHATASES PTP-D1
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/446,345
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 08/234,440
FILING DATE: 28-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: 0.2...
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
medium TYPE: Floppy disk
medium TYPE: TBM PC compatible
TOWNITER: TBM PC compatible
TOWNITER: TBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7683-054
                                                                                                                                                                                Sequence 37, Application US/08446345 Patent No. 5831009 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 76:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212) 869-8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 42.0 Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                               232 LQ 233
                                                                                    YE 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
38.9%; Score 487; DB 2; Length 24
Best Local Similarity 41.8%; Pred. No. 1.4e-49;
Matches 102; Conservative 37; Mismatches 79; Indels
                                                                                                                                                                                                                 E: HAMILTON, BROOK, SMITH & REYNOLDS, Two Militia Drive
                                                                       APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESSPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS,
                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
OPERATING SYSTEM: Windows 95
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSHL96-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/685,992
FILING DATE: 25-JUL-1996
Sequence 21, Application US/08685992
Patent No. 5912138
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CS
TELECOMMUNICATION INFORMATION
TELEPHONE: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
PILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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5, Application US/08348006B
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Best Local Similarity
Matches 100; Conserv
                                    GENERAL INFORMATION:
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                                                                                                                                                                                                               RAHWAY
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                                                                                                                                                                                  ADDRESSEE:
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US-08-800-825A-5
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   Sequence 5,
Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLVHCSAGVGRIGVFICVDVVFSALEKNYSFDIMNIVTOMRKORCGMIQTKEQYQFCYEI 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 QNLDKORYKXVDVLPYDTTRVLLQGNEDYINASYVNMEIPAANLVNK----YIATQGPLPH 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---RIVNHEEEYFYIATQGPLPE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 38.9%; Score 487; DB 2; Length 242; Best Local Similarity 41.8%; Pred. No. 1.4e-49; Matches 102; Conservative 37; Mismatches 79; Indels
                                                                  GENERAL INFORMATION:
APPLICANT: Tonks, Nicholas
APPLICANT: Filint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QNRDKNRYRDILPYDSTRVPLGKNKDYINASYI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-03Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,992
AFILING DATE: Unly 25, 1996
AFTORNEY AGENT INFORMATION:
NAME: Granahan, Patricia
                                  Sequence 21, Application US/09144925 Patent No. 5951979
                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                     Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                ZIP: 02421-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si:
                                                                                                                                                                                                              STREET: Two Milli
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ILRV 241
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                    US-09-144-925-21
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                                                                                                                                                                                                                                                                   COUNTRY:
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RESULT 13 US-08-348-006B-5

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60 QMVLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVF-LETFHVTQYFTVRV 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVGRTGVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 KNRYRDILPYDSTRVPLG----KNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.6%; Score 483.5; DB 1; Length 1911; 42.0%; Pred. No. 7.7e-48; ative 44; Mismatches 79; Indels 15;
APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: RUTLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
ORRESPONDENCES.
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,006B
                                                                                                                                                                      126 B. LINCOLN AVE., P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,032
FILING DATE: 14-5EP-1993
ATTORNEY/AGENT INFORMATION:
NAME: HAND, J., MARK
REGISTRATION NUMBER: 36,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18992IA
                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 18 TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: RODAN, AZHEL
APPLICANT: SCHMIDT, AZHEL
APPLICANT: RUTLEDGE, SU JANE
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COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
TYPE: Floppy disk
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Sequence 5. Application US/09158657
Settent No. 6214564
GENERAL INFORMATION:
APPLICANT: RODAN, GIDEON A.
APPLICANT: SCHMIDT, AZRIEL
APPLICANT: WILLEDGE, SU JANE
TITLE OF INVENTION: CDNA ENCODING A NOVEL HUMAN PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASE
CDNA ENCODING A NOVEL HUMAN PROTEIN TYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                 SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,825A FILING DATE: 14-FEB.1997 CLASSIFICATION: 435 ATTONREY/AGENT INFORMATION:
NAME: HAND, J. MARK REGISTRATION NUMBER: 36,545 REBRENCE/POCKET NUMBER: 18992DA TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 483.5; DB 2
Pred. No. 7.7e-48;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: J. MARK HAND - MERCK & CO., INC.
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
                                                                       3: J. MARK HAND - MERCK & CO., INC
126 E. LINCOLN AVE., P.O. BOX 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44; Mismatches
                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                        CORRESPONDENCE ADDRESS:
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USA
 TITLE OF INVENTION: 3
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sin
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                                                                                           STREET: 126 E
CITY: RAHWAY
                                                                                                                                                 USA
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US-09-158-657-5
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1671 KNRLVNIMPYESTRVCLQPIRGVEGSDYINASFID--GYRQQKAYIATQGPLAETTEDFW 1728
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/158,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.6%; Score 483.5; DB 3 42.0%; Pred. No. 7.7e-48;
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                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/800,825
FILING DATE: 14-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                   NAME: HAND, J. MARK
REGISTRATION NUMBER: 36,545
REPRENCE/DOCKET NUMBER: 1893
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-4720
TELEFAX: 732-594-4720
                                                                                                                                                                                                                                                                                                         36,545
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1911 amino acids
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Best Local Similarity 42.0%
Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear;
; MOLECULE TYPE: protein
US-09-158-657-5
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STRANDEDNESS: sin
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CLASSIFICATION:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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December 1, 2004, 12:07:39 ; Search time 81.7544 Seconds	(without alignments)	
Run on:		

1022.379 Million cell updates/sec US-09-095-478A-5_COPY_188_420 1253 1 QNRDKNRYRDILPYDSTRVP......MIQTKEQYQFCYEIVLEVLQ Title: Perfect score:

233

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

2002273 seqs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

geneseqp1980s; *
geneseqp1980s; *
geneseqp2000s; *
geneseqp2001s; *
geneseqp2001s; *
geneseqp2003as; * Geneseq 23Sep04:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aaw89249 Mouse PTP	0 Mouse		Human	4 Human	Human				Novel	Human			Amino	Amino	Human	Aaw75999 Intracell	Aav90272 Human PTP	Amino	Human		Human	Rat DT		Adf43232 Mouse PTP
SUMMARIES	ID	AAW89249	AAW89250	AAW89251	AAE37994	AAE14454	ABG30845	ADD89795	ADE09123	ADE08106	ABG06042	AAE37996	ADK71863	ABU70688	AAG67637	AAG67458	AAR71498	AAW75999	AAY90272	AAB19343	ADJ69543	ADL27685	ADM53457	AAW89252	ADI17283	ADF43232
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Ado55173 Protein #	Adf43234 Human PTP	Aaw12522 Protein t	Aay25156 Human PTP		Add22982 Human pro	Adl16189 Human pro	Human	Human	Human	Human	Add47019 Human Pro	Add47015 Human Pro	Adl16191 Human pro	Aag78282 Human PTP	Human	Aaw27225 Human pro	٠.		Adn02662 Liver dis
AD055173	ADF43234	AAW12522	AAY25156	AAG79333	ADD22982	ADL16189	ADF43230	ADD18742	ADE57117	ADE57121	ADD47019	ADD47015	ADL16191	AAG78282	AAR71726	AAW27225	AAW94027	AAU01459	ADN02662
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39.9	39.8	39.8	39.8	39.8	39.8	39.8	39.8	39.0	39.0	39.0	39.0	39.0	38.9	38.9	38.6	38.6	38.6	38.6	38.5
200	499	499	499	499	499	499	499	488.5	488.5	488.5	488.5	488.5	488	487	483.5	483.5	483.5	483.5	482.5
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease.
             AAW89249 standard; protein; 426 AA.
                                                                                                                                                                    97US-0044428P.
97US-0047222P.
97US-0049477P.
97US-0049956P.
97US-0063595P.
                                                                                                                                                       98WO-US008439
                                         (first entry)
                                                                                                                          WO9849317-A2
                                                                                                                                                       27-APR-1998;
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                                          10-MAR-1999
                                                         Mouse PTP05.
                                                                                                                                                                             20-MAY-1997;
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                           AAW89249;
                                                                                                           Mus sp.
RESULT 1
      AAW89249
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(SUGE-) SUGEN INC.

Markby Onrust S, Peles E, Jallal B, Hui TH; Plowman GD, Clary D, J Courtneidge SA, App H,

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WPI; 1999-009434/01. N-PSDB; AAV81744 New nucleic acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.

Claim 2; Page 155-157; 193pp; English.

The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The present sequence represents mouse PTP05. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPS) and are used to identify

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substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
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                                                                                                                                                                                                                                                               Gaps
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100.0%; Pred. No. 7.8e-136;
live 0; Mismatches 0;
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, Hui TH;
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97US-0049477P.
97US-0049756P.
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Courtneidge SA, App H,
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Best Local Similarity
                                                                                                                                                                                                         Sequence 426 AA;
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11-JUN-1997;
18-JUN-1997;
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N-PSDB; AAV81745

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The present invention describes isolated, enriched or purified nucleic acids encoding PTPO4, SAD, PTPO5, PTP10, ALP and ALK-7 proteins. The present sequence represents mouse PTPO5. The above proteins. The CALK-7, are protein tyrosine phosphatases (PTP9) and are used to identify substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and that involve the proteins particularly cancer (e.g. leukaemia and serine/threonine kinase) are used to promote neuronal survival.

CC particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polymouleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
         New nucleic acid encoding specific protein tyrosine phosphatases - u for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VFICVDVVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYBIVLEVLQ 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1253; DB 2;
100.0%; Pred. No. 8.8e-136;
ive 0; Mismatches 0;
                                                                                     Page 157-158; 193pp; English
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97US-0047222P.
97US-0049477P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 463 AA;
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11-JUN-1997;
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acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 processors acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 processors. The present sequence represents mouse PTP05. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTP8) and are used to identify substances that modulate their activity (1.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor scrine/threonine kinase) are used to promote neuronal survival, and iseases. Nucleic acid fragments of the polynucleotides encoding the proteins and be used as probes to identify and clone related sequences; to detect protein-encoded RNA, to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis; atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer; psortasis; thrombocytopaenia; developmental disorder; Reiter's syndrome; renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease; neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis;
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                                                                                                                                                                                                                                                                                                                                 present invention describes isolated, enriched or purified nucleic
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                                                                                                         Markby
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Pred. No. 1e-126;
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                                                                                                         Peles
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                                                                                                                                                                                                                                                          cancer and neurodegenerative disease.
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97US-0049756P.
97US-0049914P.
                                    97US-0063595P
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Best Local Similarity 100.
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                                                                       SUGE-) SUGEN INC.
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11-JUN-1997;
                                    23-OCT-1997;
                   18-JUN-1997;
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                                                                                                             Plowman GD,
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autoimmune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome; acquired immune deficiency syndrome; immunosuppressive; Crohn's disease; nostropic; transgenic; dermatitis; multiple sclerosis; diabetes mellitus; allergy; gout; Grave's disease; Hashimoto's thyroiditis; bowel syndrome; osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological; gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.

Homo sapiens.

WO2003050084-A2

19-JUN-2003.

nseful

06-DEC-2002; 2002WO-US039126.

07-DEC-2001; 2001US-0340235P. 19-DEC-2001; 2001US-034307P. 21-DEC-2001; 2001US-0343546P. 04-FEB-2002; 2002US-0354388P.

15-FEB-2002; 2002US-0357675P.

(INCY-) INCYTE GENOMICS INC

JA, Marquis JP; Hawkins PR; Gorvad AE; , Griffin JA, R, Lee S, Haw Wilson AD, Swarnakar A, Go ling BM, Ramkumar J, Jin P, ' NX, Lehr-Mason PM, Khare R, Sprague WM, Zebarjadian Y; Hafalia AJA, Emerling BM, Baughn MR, Chawla NK, Le} Hatair Baughn MR, Charr So, Lee SY, Chien D, Kable AE,

WPI; 2003-532894/50. N-PSDB; AAD57366.

New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis, cancer or hepatitis.

Claim 1; Page 242; 282pp; English.

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syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral, bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP is useful in assessing the effects of exogenous compounds on the expression of nucleic acids and kinases and phosphatases. KPP gene is useful in gene therapy and for creating transgenic animals to model human disease. The present sequence is human KPP protein The invention relates to an isolated polypeptide, which is a human kinase and phosphatase (KPP). KPP agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of KPP, particularly cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis, cirrhosis, hepaticis, parcxysmal neemoglobinuria, polycythaemia vera, psoriasis, primary thromobocycopaemia or cancer), developmental disorders (eg. renal thromobocycopaemia or mental retardation), neurological disorders (e.g. Allzehmer's disease, Parkinson's disease or epilepsy), autoimmune/inflammatory disorders (e.g. AllDs), aqquired immune deficiency syndrome, allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease, diabetees melliture, glomerulonephritis, Godpasture's syndrome, gout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome, multiple sclerosis, osteoporosis, pancreatitis, Reiter's

Sequence 261 AA;

Gaps , 0 80.0%; Score 1003; DB 6; Length 261; 78.9%; Pred. No. 3.5e-107; Indels 25; 24; Mismatches 183; Conservative Query Match Best Local Similarity

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61 83 NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEBEYFYIATQGPLPETIEDFWQM

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VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEPEHFSVFLETFHVTQYFTVRVFQI 121 62

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TALLON, SEVERE COMBINED INTERPRETATION, AUGUSTA, AUGUSTA, SEVERE COMBINED INTERPRETATION, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUGUSTA, AUG
severe combined immunodeficiency disease (SCID), adult
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Tang YT, Thornton M;
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                             VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; protein phosphatase; PP-4; immune system disorder; AIDS; allergy; neurological disorder; developmental disorder; Alzheimer's disease; cell prolliferative disorder; Huntington's disease; arteriosclerosis; renal tubular acidosis; gonadal dysgenesis; cancer; adenocarcinoma; leukaemia; transgenic animal; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Griffin JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Tyrosine specific protein phosphatase active
                                                                                                                              FICUDIVIESALEKNYSFDIMNIVIQMRKQRCGMIQTKEQYQFCYEIVLEVLQ
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/note= "Protein-tyrosine phosphatase"
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Kearney L, Lee EA, Lu Y, Nguyen DB,
Reddy R, Sanjanwala MS, Stewart EA,
M, Walia NK, Yang J, Yao MG, Yue H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                     AAE14454 standard; protein; 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0213746P.
2000US-0215210P.
2000US-0216529P.
2000US-0218080P.
2000US-0220117P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein phosphatase-4.
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                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Hafalia A, F
Ramkumar J,
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                                                                                                      182
                                                   144
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                                                                                                                                                                                                                                  RESULT 5
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                                                                                                                                           VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; tyrosine phosphatase; obesity; diabetes; Parkinson's disease; central nervous system disorder; CNS; cardiovascular disorder; stroke; chronic obstructive pulmonary disease; cancer; multiple sclerosis; Alzheimer's disease; Huntington's disease; congestive heart failure; myocardial infarction; chromosome 10.
                                                                                              183 NREKNRYRDILDYDSTRVPLGKSKDYINASYIRIVNCGEEYFYIATQGPLLSTIDDFWQM
                                                                                                                                                                  243 VLENNSNVIAMITREIBGGIIKCYHYWPISLKKPLELKHFRVFLENYQILQYFIIRMFQV
                                                                                                                                                                                                                                        NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQM
                                                                                                                                                                                                                   VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV
                                     Gaps
                                                                                                                                                                                                                                                                                         182 FICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ 233
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80.0%; Score 1003; DB 5; Length 420; 78.9%; Pred. No. 7e-107; ive 24; Mismatches 25; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human tyrosine phosphatase protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                      ABG30845 standard; protein; 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                     183; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2002.
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The present sequence is human protein phosphatase (PP)-4. PP polymuclectide and polypeptide are useful in the diagnosis, treatment and prevention of immune system disorders, neurological disorders, developmental disorders and cell proliferative disorders. Examples of immune system disorders include acquired immune deficiency syndrome

Claim 1; Page 105-106; 116pp; English.

endometriosis; angiogenesis.

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The present invention relates to a new human tyrosine phosphatase

Co polypeptide. The invention is useful for the preparation of a medicament

Co for modulating the activity of human tyrosine phosphatase in a disease

Such as obesity, diabetes, a central nervous system (CNS) disorder,

Co fronic obstructive pulmonary disease, cardiovascular disorder or cancer.

Co fronic obstructive pulmonary disease, cardiovascular disorder or cancer.

Co free invention is useful for treating a human tyrosine phosphatase

Co five invention is useful for treating the above mentioned diseases. The

invention is useful for treating the above mentioned diseases. The

CNS disorder is selected from Parkinson's disease, and the

cordiovascular disorder is selected from congestive heart failure and

cordiovascular disorder is selected from congestive heart failure and

confidential infarction. The molecules of the invention are useful in

cliagnostic assays for detecting diseases and abnormalities or

cusceptibility to disease and abnormalities related to the presence of

susceptibility to disease and abnormalities related to the presence of

mutations in the polymucleotide coding the polymeptide of the invention.

The present amino acid sequence represents the human tyrosine phosphatase

cordiovascular disvance of chromosome 10

cy tyrosine phosphatase gene located on chromosome 10
                                                                                                                                                                                                                                           New human tyrosine phosphatase polypeptide, the regulation of which is useful for treating obesity, diabetes, cardiovascular or central nervous system disorder, chronic obstructive pulmonary disease and cancer.
                                                                                                                                                                                                                                                                                                                                                                  Claim 25; Fig 2; 145pp; English
27-NOV-2000; 2000US-0252912P.
                                                                                                                                                                  WPI; 2002-575236/61
                                                    (FARB ) BAYER AG
                                                                                                                                                                                               N-PSDB; ABK89178
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Sequence 398 AA;

220 61 161 NREKNRYRDILPYDSTRVPLGKSKDYINASYIRIVNCGEEFFYIATQGPLLSTIDDFWQM VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQM Gaps FICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYBIVLEVLQ 233 .; 0 Length 398; Indels 25; 79.4%; Score 995; DB 5; I 78.0%; Pred. No. 5.5e-106; iive 26; Mismatches 25; Matches 181; Conservative Best Local Similarity 341 a 182 62 Query Match 셤 엄 g ò ò δ

cancer associated phosphatase; enzyme; human; cancer; tumour; cytostatic; immunosuppressive; antidiabetic; neuroprotective; antirheumatic; antiarthritic; antipsoriatic; antiarteriosclerotic; antiinflammatory; vulnerary; gynaecological; antiangenic; hyperproliferative disease; autoimmune disease; diabetes mellitus; multiple sclerosis; rheumatoid arthritis; psoriasis; atherosclerosis; inflammation; scarring; Human DKFZP566K0524 protein SEQ ID NO:10. Z ADD89795 standard; protein; 398 (first entry) 29-JAN-2004 ADD89795 RESULT 7

Sequence 398 AA;

invention

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New nucleic acids encoding cancer associated phosphatases, useful as targets for screening pharmaceutical agents that inhibit the growth tumor cells, or for diagnosing and treating cancer, inflammation or
                                                         28-MAR-2002; 2002US-0368859P.
                                             19-MAR-2003; 2003WO-CA000393.
                                                                      (KINE-) KINETEK PHARM INC.
                                                                                             WPI; 2003-902934/82.
                                                                                                                                 autoimmune disease.
                                                                                                    N-PSDB; ADD89794
                      WO2003083102-A2.
            Homo sapiens.
                                   09-OCT-2003
                                                                                  Delaney AD;
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Claim 1; SEQ ID NO 10; 63pp; English

purplanease of the present invention mass cycleater, immensional presents, antidabetic, neuroprotective, antirhenmatic, antidarthic, antidateric, and antidated and antidated and antidated and treating cancer, e.g. paraceas, lung, ovarian, liver or colon cancer. The polypeptides and nucleic acids may also be used for treating hyperproliferative diseases, cuch as autoimmune disease, diabetes mellitus, multiple sclerosis, rheumatoid arthritis, psoriasis, atherosclerosis, inflammation, scarring, endometriosis or angiogenesis, determining the effectiveness of drugs, determining patient prognosis, or as targets for screening pharmaceutical agents that inhibit the growth or metastasis of tumour cells. The present sequence represents the human cancer associated phosphatase The present invention describes an isolated cancer associated phosphatase nucleic acid. Also described: (1) a method of screening for biologically active agents that modulate a cancer associated phosphatase function; (2) a method for the diagnosis of cancer; (3) a method for inhibiting the growth of a cancer cell; (4) methods of screening for targets of a cancer associated phosphatase, where the targets are associated with signal transduction in cancer cells; (5) a compound (C) for the treatment of a tumour; (6) a composition for the treatment of a tumour comprising a pharmaceutical carrier and (C); (7) methods for treating a tumour; and (8) a method for visualising a tumour in a patient. A cancer associated phosphatase of the present invention has cytostatic, immunosuppressive,

ö 281 VEKSTGTSHSVKQLQFTKWPDHGTPASADSFIKYIRYARKSHLTGPWVVHCSAGIGRTGV 340 121 181 61 122 VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV 2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQM VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI Gaps ; 0 Length 398; Indels 79.4%; Score 995; DB 7; I 78.0%; Pred. No. 5.5e-106; iive 26; Mismatches 25; Best_Local Similarity 78.08
Matches 181; Conservative 62 Query Match q g δ 유 à

FICVDVVFSAIEKNYSFDIMNIVTQMFKQRCGMIQTKEQYQFCYEIVLEVLQ 233

182

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271 NREKNRYRDILDYDSTRVPLGKSKDYINASYIRIVNCGEEYFYIATQGPLLSTIDDFWQM 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed, as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence represents a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATOGPLPETIEDFWOM
                                                                                                                                                                                                                                                                                        novel gene; novel protein; tissue marker; molecular weight marker; chromosome marker; genetic disorder.
                                       182 FICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ
                                                                                                                                                                                                                                                      Novel protein (useful for identifying genetic disorders) #261.
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Drmanac RT,
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1 M, Xue AJ, Wehrman T, Weng G, Zhou P,

Wang D, Chen R, Xu C, Boyle BJ;
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78.0%; Pred. No. 7.8e-106;
iive 26; Mismatches 25;
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                                                                                                                                                Ā
                                                                                                                                              ADE08106 standard; protein; 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 2001US-0339739P.
; 2001US-0339453P.
; 2002US-036591P.
; 2002US-0365384P.
; 2002US-0372381P.
; 2002US-037261SP.
; 2002US-0012858.
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                                                                                                                                                                                                                    (first entry)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the invention.
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14-MAR-2002;
12-APR-2002;
12-APR-2002;
22-APR-2002;
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11-DEC-2001;
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Ghosh M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynuclectides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present amino acid sequence was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI
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                                                                                                                                                                                                                                     marker;
341 FLCVDVVFCAIVKDCSFNIMDIVAQMREQRSGMVQTKEQYHFCYDIVLEVLR 392
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Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 409;
                                                                                                                                                                                                                                 novel gene; novel protein; tissue marker; molecular weight chromosome marker; genetic disorder; contig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                               Novel protein-related contig polypeptide sequence #189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ren F, Zhou P,
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Pred. No. 5.7e-106;
6; Mismatches 25;
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Boyle BJ;
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                                                                                      ADE09123 standard; protein; 409
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Tang YT, Xue AJ, Wehrman T, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26;
                                                                                                                                                                                                                                                                                                                                                                                                                                 2001US-0339739P.
2001US-0339453P.
2002US-0365091P.
2002US-0365384P.
2002US-0372381P.
2002US-0372381P.
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                                                                                                                                                             (first entry)
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Chen R,
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Best Local Similarity
Matches 181; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 409 AA;
                                                                                                                                                                                                                                                                                                                         WO2003054152-A2.
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12-APR-2002; 2
22-APR-2002; 2
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14-MAR-2002;
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                                                                                                                                                             29-JAN-2004
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                                                                       ADE09123
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Wang J; lang Z;

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The invention relates to isolated polynucleotide (I) and polypeptide (II) capences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed control of the control of the control of cactivity of (II) is useful in gene therapy techniques to restore normal cactivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of supplement. (II) and its binding partners are useful for treating disorders of supplement. (II) and its binding partners are useful for treating disorders of supplement. (II) and (II) are useful for treating disorders of supplement protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in the produce of matter of genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AbG00010-ABG30377 represent novel human diagnostic canno acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in effectionic format directly from WIPO at the control of the control of the control of the control of the control of the control of the control of calculation of calculation of calculation of calculation of calculations.
                                           450
      181
VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV
                       New isolated polymucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                 Human, chromosome mapping, gene mapping, gene therapy; forensic
food supplement, medical imaging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 36401; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                          Novel human diagnostic protein #6033
                                                                                                                                                                                                                                    ABG06042 standard; protein; 561 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                        (first entry)
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            122
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                                                   셤
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Length 561;

DB 4;

79.4%; Score 995;

Query Match

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Gorvad AE;
Griffin JA, Marquis JP;
R, Lee S, Hawkins PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; kinase; phosphatase; KPP; cell proliferative disorder; hepatitis; atherosclerosis; cirrhosis; haemoglobinuria; polycythaemia vera; cancer; psoriasis; thromobocytopaenia; developmental disorder; Reiter's syndrome; renal tubular acidosis; anaemia; mental retardation; Alzheimer's disease; neurological disorder; Parkinson's disease; epilepsy; glomerulonephritis; acquired immune disorder; inflammatory disorder; AIDS; Goodpasture's syndrome; acquired immune deficiency syndrome; immunosuppressive, Crohn's disease; allergy; gout; Grave's disease; Habhinoto's thyroiditis; bowel syndrome; osteoporosis; rheumatoid arthritis; Sjogren's syndrome; ophthalmological; gene therapy; asthma; anticonvulsant; uropathic; pancreatitis.
                       0
                                                                                                                                                                181
                                                                  VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEFEHFSVFLETFHVTQYFTVRVFQI 121
                                                                                                                          New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis, cancer or hepatitis.
                                                   61
                                                                                                                                                               VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIXYVRYVRXSHITGPLLVHCSAGVGRTGV
                                                  2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATGGPLPETIEDFWQM
                                                                                                                                                                                                                                    ..
                                                                                                                                                                                                                       FICVDVVFSAIBKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVLQ
                          Indels
9e-106;
25;
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A, Emerling BM, Ramkumar J, Jin P,
Chawla NK, Lehr-Mason PM, Khare R,
Lee SY, Sprague WW, Zebarjadian Y;
                                                                                                                                                                                                                                                                                                                                                                                                           Human kinase and phosphatase (KPP-41) protein.
              78.0%; Pred. No. 9e-1
ive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 243-244; 282pp; English
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                                                                                                                                                                                                                                                                                                                             AAE37996 standard; protein; 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-2001; 201US-0343007P.
21-DEC-2001; 2001US-0343546P.
04-FEB-2002; 2002US-0354388P.
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Hafalia AJA, Emer....
Baughn MR, Chawla NK,
Tee SY, Spr?
                             181; Conservative
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                 Similarity
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                 Best Local
                                Matches
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Tran UK;

Richardson TW, Marquis JP, Swarnakar A, Tang YT, Emerling BM, Jin P, Wilson AD, Yue H, Gietzen KJ; Kang YG, Lee SY, Khare R, Elliott VS, Hafalia AJA; Ramkumar J, Gururajan R, Tribouley CM, Chien D,

Yang YG,

Chang H,

26-AUG-2002; 2002US-0406172P. 25-SEP-2002; 2002US-0413910P. 27-SEP-2002; 2002US-0414296P. 11-OCT-2002; 2002US-0417821P.

(INCY-) INCYTE CORP.

Baughn MR, Becha SD, Chawla NK, Murage J; New human kinases and phosphatases, useful for diagnosing, treating or preventing atherosclerosis, hypertension, AIDS, allergy, multiple sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer

WPI; 2004-226830/21. N-PSDB; ADK71922.

Claim 1; SEQ ID NO 40; 347pp; English.

or hepatitis.

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The Invention relates to an isolated polypeptide, winch is a numan kinase and phosphataee (KPP). KPP agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of KPP, particularly cell proliferative disorders (e.g. arteriosclerosis, atherosclerosis, cirhosis, hepatitis, paroxysmal nocturnal haemoglobinuria, polycythemia vera, psoriasis, primary thrombocytopaenia or cancer) developmental disorders (eg. renal tubular acidosis, anaemia or mental retardation), neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or epilepsy), autoimmune, allergise, sathma, autoimmune thyroiditis, contact dermatitis, Crohn's inflammatory disorders (e.g. AIDS; acquired immune deficiency syndrome, allergise, sathma, autoimmune thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus, glomeriolomephritis, Goodpasture's syndrome, cout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome, cout, Grave's disease, Hashimoto's thyroiditis, irritable bowel syndrome, bacterial, fungal, parasitic, protozoan or helminthic infections. The KPP contental, fungal, parasitic, protozoan or helminthic infections. The KPP contental, in gene therapy and for creating transgemic animals to model human contents. The present sequence is human KPP protein
   invention relates to an isolated polypeptide, which is a human kinase
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Sequence 412 AA;

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183 NREKNRYRDILPYDSTRVPLGKSKDYINASYIRIVNCGEEYFYIATQGPLLSTIDDFWQM 242
                                                                                                                       121
                                                                                                                                243 VLENNSNVIAMITREIEGGIIKCYHYWPISLKKPLELKHFRVPLENYQILQYFIIRMFQV 302
                                                                                                                                                                         VKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRTGV 181
                                                                                                                                                                                          61
                                                         2 NRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHEEEYFYIATQGPLPETIEDFWQM
                                                                                                                 VLENNCNVIAMITREIECGVIKCYSYWPISLKEPLEPEHFSVFLETFHVTQYFTVRVFQI
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    6; Length 412;
                                 24; Indels
                                                                                                                                                                                                                                   FICUDUVESALEKNYSFDIMNIVTQMRKQRCGMIQTKE 219
                                                                                                                                                                                                                                                    Score 941; DB 6
Pred. No. 1e-99;
                              22; Mismatches
75.1%;
78.9%;
                               Conservative
                Local Similarity
                            Matches 172;
                                                                                                                                                                                                                                                                363
                                                                                                                 62
                                                                                                                                                                           122
                                                                                                                                                                                                                                   182
   Query Match
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human; kiname; phosphatase; KPP; cardiovascular; antiarteriosclerotic; hypotensive; vasotropic; antialflammatory; antianginal; anti-HIV; antialsthmatic; immunosuppressive; antithyroid; dermatological; antidabetic; nephrotropic; antigout; gastrointestinal; neuroprotective; osteopathic; nephrotropic; antigout; gastrointestinal; antirhematic; antiparkinsonian; nootropic; anticonvulsant; hepatotropic; antiparmatic; namiparatic; cytostatic; antiparmic; antiparmitic; antipartic; cytostatic; antiparmitic; antiparatic; cytostatic; antiparmitic; antiparatic; cardiovascular disease; immune system; neurological; growth, development; cell proliferation; viral; bacterial; fungal; parasitic; protozoan;
                                                                                                                                                                                                                                                                                                                                                     cell proliferation; viral; vaccell, ..., enzyme.
                                                                                                                                                Human kinase and phosphatase KPP-40 protein.
                                     ADK71863 standard; protein; 348 AA.
                                                                                                             (first entry)
                                                                                                             20-MAY-2004
                                                                        ADK71863:
                                                                                                                                                                                                                                                                                                                                                                                                             Homo
RESULT 12
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ABU70688 standard; protein; 766 AA

ABU70688

ABU70688;

25-AUG-2003; 2003WO-US026635.

WO2004018641-A2 sapiens

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The invention relates to a novel isolated polypeptide which is a human kingse and phosphatase (KPP). The polypeptide of the invention demonstrates cardiovascular, antiantianological to the invention antialiammatory, antianginal, antiallargic, antialiametory, antianginal, antiallargic, antialiabetic, nephrotropic, antigout, gastrointestinal, neuroprotective, cartialpatric, nephrotropic, antigout, gastrointestinal, neuroprotective, osteopathic, antiarthritic, uropathic, ophthalmological, antiparkinsonian, nootropic, antionwalsant, hepatotropic, antipsoriatic, antiparkinsonian, nootropic, antionwalsant, hepatotropic, antipsoriatic, antipacterial, virucide, protozoacide and fungicide activities. The kinase and phosphatase (KPP) polynucleotides, polypeptides, agonists and antibacterial, virucide, protozoacide and fungicide activities. The kinase and phosphatase (KPP) polynucleotides, polypeptides, agonists and antibacterial, virucide, protozoacide and diseases; immune system disorders, or proliferative disorders and diseases; immune system disorders, protozoan or helminthic infections. Furthermore, the molecules of the invention may be useful for creating transgenic animals to model human to be not the herapy. The current sequence is that of a human to be human and an animals to model human to be hospitally and animals to model human to be hospitally and animals to model human to be hospitally and animals and animals and animals and animals and animals and animals and animals and animals and animals and animals and animals and animals and animals and animals and animals and animals and animals and animals and animals and animals and animals animals animals animals and animals animals animals and animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animals animal
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Human adipocyte Selected Interacting domain, SID, #319.
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                                                                          14-MAR-2001; 2001US-0275734P.
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(first entry)
                                                                                                                    New complex between two
                                                                                             Legrain P, Daviet L;
                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                              interactions, or for
obesity or diabetes.
                                                                                    (HYBR-) HYBRIGENICS.
                                                                                                      WPI; 2003-103412/09.
                                                                                                                                                                                                                                                                      Sequence 766 AA;
                                                                                                           N-PSDB; ACA57232
                                                                                                                                                                                                                                                                                        111;
                                      Homo sapiens.
LO-JUN-2003
                                                        31-OCT-2002.
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Best Local S
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WO200109316-A1.
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                                                                                                                 AAG67637;
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Ishii S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                 RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a complex between two interacting proteins in adipocyte cells, given in the specification. The proteins are identified by selecting a bait protein from a known adipocyte marker and then by selecting a bait protein from a known adipocyte marker and then ce performing a yeast 2-hybrid selection to isolate prey proteins encoded by members of an adipocyte cDNA library. The proteins are designated SID (RTM) (selected interacting domains) proteins. Also included are a polypeptide in the adipocyte cells, a polypeptide encoding a polypeptide in the adipocyte cells, a ceombinant host cell expressing at least one of the interacting polypeptides of the complex, selecting a modulating compound in adipocyte cells, a SID (RTM) polypeptide comprising any of the 738 amino acid sequences given in the specification (including its fragmen to variant), a vector comprising the vector, a protein cincluding its fragmen to variant, a vector comprising the vector, a protein comprising the polypeptides and a recomblex, polypeptides, polymucleotides and compounds are useful for comprising or treating metabolic disorders such as obesity or diabetes. The polymucleotides are useful for granting or treating metabolic disorders such as obesity or diabetes. The polymucleotides are useful as probes or primers. The complex is probes or primers. The complex is carried remained drugs that medulate the protein interaction, thus complexing the therapeutic effect. The present sequence represents a SID (Rrw) protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                 complex between two interacting proteins in adipocyte cells, useful identifying selected interacting domains that modulate protein stactions, or for preventing or treating metabolic disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QIVKKSTGKSQCVKHLQFTKWPDHGTPASADFFIKYVRYVRKSHITGPLLVHCSAGVGRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Human, prey, adipocyte, SID, selected interacting domain, anorectic, antidiabetic, protein-protein interaction, diabetes, yeast 2-hybrid assay, metabolic disorder; obesity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.3%; Score 592.5; DB 6;
47.6%; Pred. No. 6e-59;
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1078 MIWEQKSTVIAMMIQEVEGEKIKCORYWPNILGKTTWVSNRLRLALVRMQQLKGFVVRAM 1137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The specification describes human protein kinase/protein phosphatases. It is expected that the protein kinase/protein phosphatase gene participates in signal transduction in cells. The protein kinase/protein phosphatase polypeptides and polymucleotides are useful for developing diagnostics and treatment agents for human and animal diseases. The protein kinase/protein phosphatase polypeptides are useful as target molecules in designing novel drugs. The protein kinase/protein phosphatase polypeptides are useful as target molecules in polymucleotides are useful as a source of probes and primers, which may be used to isolate homologous sequences. The present sequence represents a human protein, which is used in the course of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New genes encoding proteins with protein kinase/protein phosphatase activity, useful in the diagnosis and treatment of diseases.
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                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                           Human; protein kinase; protein phosphatase; signal transduction.
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47.6%; Pred. No. 1.2e-58;
Live 41; Mismatches 80; Indels 1;
180 GVFICVDVVFSAIEKNYSFDIMNIVTOMRKORCGMIQTKEQYQFCYEIVLEVL
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, Otsuki T,
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A, Nagai K,
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                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a human protein.
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T, Wakamatsu
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                                                                                                                                                                                                         AAG67637 standard; protein; 1267
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11-JAN-2000; 2000JP-00118776.
17-FEB-2000; 2000US-0183322P.
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Nezu J:
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180 GVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYQFCYEIVLEVL
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1138 TLEDIQTREVRHISHLNFTAWPDHDTPSQPDDLLTFISYMRHIHRSGPIITHCSAGIGRS 1197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The polypeptides are expected to participate in signal transduction in cells. The kinase phosphatases are connected with intracellular signalling pathways. Antisense oligonucleotides and compounds identified by screening (agonists or antagonists) can be used to treat human or animal disorders associated with the expression or function of the protein. In addition, the polypeptides may be used as target molecules fir drug development. The present sequence represents a polypeptide, used in the course of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ONRDKNRYRDILPYDSTRVPLGKNKDYINASYIRIVNHBEEXFYIATQGPLPETIEDFWQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saito K, Yamamoto J;
Otsuki T, Funahashi S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New genes encoding protein kinase and protein phosphatase, useful for identifying modulators which can be used to treat human or animal disorders associated with the expression or function of these enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The specification describes human protein kinase/protein phosphatases
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                                               232
                                                                                                                                                                                                                                                       Human; protein kinase; protein phosphatase; signal transduction; intracellular signalling pathway.
                             GVFICVDVVFSAIEKNYSFDIMNIVTQMRKQRCGMIQTKEQYOFCYEIVLEVL
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47.6%; Pred. No. 1.2e-58;
tive 41; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                            Amino acid sequence of a human polypeptide.
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                                                                                                                                    AAG67458 standard; protein; 1267
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Sugiyama T, Wakamatsu
Nezu J;
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18-OCT-1999; 99US-0159590P.
11-JAN-2000; 2000JP-00118776.
17-FEB-2000; 2000US-0183322P.
                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000; 2000WO-JP005060
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Best Local Similarity 47.6%
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Ishii S,
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